

-15					-10					-5					
Gly	Gly	Glu	Ile	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	His	Ser
		1				5					10				
Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	Leu	Leu	Trp
15					20					25					30
Gly	Asp	Ala	His	Arg	Pro	Gln	Met	Ala	Pro	Asp	Ser	Ser	Pro	Leu	Pro
				35					40					45	
Gln	Ala	Pro	Leu	His	Ser	Ser	Pro	Gly	Ala	Ala	Gln	Pro	Pro	Glu	Gly
			50					55					60		

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -38..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.4
 seq LWLLKLKLVSTXWA/VR
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Met Leu Glu Glu Cys Gly Ala Gly Val Asp Leu Gly Phe Gly Gly Val  
-35 -30 -25

-

Lys Phe Ala Ser Glu Thr Pro Asn Leu Leu Trp Leu Leu Leu Lys Leu  
-20 -15 -10

Val Ser Thr Xaa Trp Ala Val Arg Val Thr Leu Ile Ile Phe Asn Asn  
-5 1 5 10

Gln Ala Arg

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Normal prostate

- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -23..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 10.2  
                            seq RCLLLALVAESSS/QT

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Ile Ala Cys Ser Ile Arg Glu Leu His Arg Cys Leu Leu Leu Ala  
      -20                    -15                    -10  
  
Leu Val Ala Glu Ser Ser Ser Gln Thr His Gly  
      -5                            1

- (2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: PROTEIN  
  
(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Cancerous prostate  
  
(ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -17..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 10.2  
                            seq SLVLCLLSATVFS/LQ

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe  
      -15                    -10                    -5  
  
Ser Leu Gln Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Pro Gly  
      1                            5                    10                    15

- (2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 112 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9  
seq AMWWLLWGVQLQX/XP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp Arg Ser Pro His  
-35 -30 -25 -20

Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu Leu Trp Gly Val  
-15 -10 -5

Leu Gln Xaa Xaa Pro Asn Pro Gly Leu Arg Pro Leu Gly Xaa Arg Ala  
1 5 10

Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala Val Trp Gln Arg  
15 20 25

Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly Leu Cys Cys Glu  
30 35 40 45

Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro Gly Leu Cys Arg  
50 55 60

Gly Leu Cys His Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Leu Gly  
65 70 75

## (2) INFORMATION FOR SEQ ID NO: 327:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq LLTLALLGGPTWX/XK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met His Arg Pro Glu Ala Met Leu Leu Leu Thr Leu Ala Leu Leu  
           -20                          -15                          -10

Gly Gly Pro Thr Trp Xaa Xaa Lys Met Tyr Gly Pro Gly Gly Gly Lys  
       -5                                  1                          5                          10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg  
                           15                          20                          25

Val Ser Val Gly Xaa Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly  
                           30                          35                          40

Asp Ser Trp Asp Val Lys Leu Gly Gly Leu Arg Trp Glu Tyr Pro Gly  
                           45                          50                          55

Ser His Pro Ala Ala Arg Arg Ile His His Lys Ser Leu Cys Arg Phe  
       60                          65                          70

Gln Ala Phe Leu  
       75

## (2) INFORMATION FOR SEQ ID NO: 328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
                                                           seq SVSLALLSGWVGS/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Val Ser Val Ser Leu Ala Leu Leu Ser Gly Trp Val Gly Ser Arg  
       -15                          -10                          -5                          1

Gln Gly Gly Val Gly Leu Ser Thr Leu Val Thr Leu Gly Leu Val Ser  
                           5                          10                          15

Trp Cys Trp Arg Met Val Arg Thr Gln Ala Leu Glu Gly Phe Leu Ser  
                           20                          25                          30

Val Lys Tyr Tyr Ser Ala Phe Ser Ala Asp Leu  
       35                          40

## (2) INFORMATION FOR SEQ ID NO: 329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq IVFLLLRVSPCLG/PS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

```

Met His Ile Phe Ser Ile Cys Cys Met Xaa Ser Glu Leu His Lys Met
 -45 -40 -35

Lys Ser Leu Ser Leu Gln Leu Ala Ser Glu Lys Arg Ser Leu Val Ala
 -30 -25 -20

Leu Val Glu Glu Ile Val Phe Leu Leu Arg Val Ser Pro Cys Leu
 -15 -10 -5

Gly Pro Ser Xaa Lys Pro Arg
 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 330:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq VSALLMAWFGVLS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

```

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu
 -15 -10 -5

```

Ser Cys Val Gln Thr Gly  
 1 5

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LLLPLMLMSMVSS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Pro Leu Met Leu  
 -20 -15 -10

Met Ser Met Val Ser Ser Ser Leu Xaa Pro Gly Val Ala Arg Gly His  
 -5 1 5 10

Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Leu  
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LLLPLMLMSM/SS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Pro Leu Met Leu  
           -20                          -15                          -10

Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His  
       -5                                  1                          5                          10

Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln  
                           15                                  20                                  25

Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe  
                           30                                  35                                  40

Met Thr Val Ser Gly  
                   45

## (2) INFORMATION FOR SEQ ID NO: 333:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2  
seq LLLLQLSLPSPTS/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Leu Leu Leu Leu Gln Leu Ser Leu Pro Ser Pro Thr Ser Ser Pro  
                           -10                                  -5                                  1

## (2) INFORMATION FOR SEQ ID NO: 334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1  
seq LSFKLLLLAVALG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```

Met Leu Lys Met Leu Ser Phe Lys Leu Leu Leu Leu Ala Val Ala Leu
 -15 -10 -5

Gly Phe Phe Glu Gly Asp Ala Lys Phe Gly Glu
 1 5 10

```

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq LLTLALLGXXXWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu Leu
 -20 -15 -10

Gly Xaa Xaa Xaa Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys
 -5 1 5 10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg
 15 20 25

Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly
 30 35 40

Asp Ser Trp Asp Val
 45

```

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids



(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8  
seq VSAVLCVCAAAWC/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp Cys  
-15 -10 -5

Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly Gly Arg  
1 5 10 15

Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Thr Ile  
20 25 30

Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys Phe Arg Asp Asp  
35 40 45

Asp Tyr Phe Arg Thr Gly  
50

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.8  
seq VLWLISFFFTDG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp  
-15 -10 -5

Gly His Gly Gly Phe Leu Gly Lys Asn Asp Gly Ile Lys Thr Lys Lys  
 1 5 10 15  
 Glu Leu Ile Val Asn Lys Lys Lys His Leu Gly Leu Gly  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq ILLDLICLLFITA/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Cys Ile Ile Leu Leu Asp Leu Ile Cys Leu Leu Phe Ile Thr Ala  
 -15 -10 -5  
 Cys Val Gly  
 1

## (2) INFORMATION FOR SEQ ID NO: 339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -59..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FMVFGSFFPLISC/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

```

Met Asp Cys Ala Ser Ile Ser Val Lys Phe Thr Ser Met Ala Thr Met
 -55 -50 -45
His Asp Leu Ser Gln Phe Trp Ala Ser Arg Gly Glu Val Thr Asn Trp
 -40 -35 -30
Trp Pro Val Gly Gln Thr Ser Leu Pro Leu Phe Tyr Leu Ala Phe Met
 -25 -20 -15
Val Phe Gly Ser Phe Phe Pro Leu Ile Ser Cys Gln Pro Gly
 -10 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq LVVLFGITAGATG/AK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

```

Met Thr Ala Ser Pro Asp Tyr Leu Val Val Leu Phe Gly Ile Thr Ala
-20 -15 -10 -5
Gly Ala Thr Gly Ala Lys Leu Gly Ser Asp Glu Lys Glu Leu Ile Leu
 1 5 10
Leu Phe Trp Lys Val Val Asp Leu Ala Asn Lys Lys Val Gly Gln Leu
 15 20 25
His Glu Xaa Xaa Leu Asp Arg Ile Trp
 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -15..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.6  
 seq CVLVLAAAAGAVA/VF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

```

Met Val Cys Val Leu Val Leu Ala Ala Ala Gly Ala Val Ala Val
-15 -10 -5 1
Phe Leu Ile Leu Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr
 5 10 15
Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His
 20 25 30
Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser
 35 40 45
Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met Ser Ala Thr
 50 55 60

```

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -44..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.5  
 seq LMIPLLLLTPITA/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```

Met Lys Lys Thr Gly Asp Gly Gly Thr Leu Ser Thr Glu Arg Ile Gly
 -40 -35 -30
Gly Ala Ala Leu Leu Ser Leu Leu Lys Arg Met Lys Met Thr Leu
 -25 -20 -15

```

Met Ile Pro Leu Leu Leu Leu Thr Pro Ile Thr Ala Thr Ser Thr Ser  
           -10                              -5                              1

Arg Trp Pro Glu Ile Gly Val Val Ala Ile Arg Ser Gln Leu Arg Ala  
   5                              10                              15                              20

Leu His Thr Cys Gly Gln Glu Pro Val Pro Ala Met Gly Ser Glu Gly  
                               25                              30                              35

Ala Ala

## (2) INFORMATION FOR SEQ ID NO: 343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5  
seq LTFLQLLLISSLP/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Leu  
                               -20                              -15                              -10

Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn Glu Ala  
                               -5                              1                              5

Cys Pro Gly Ala Glu Trp Xaa Ile Met Cys Arg Glu Cys Cys Glu Tyr  
   10                              15                              20                              25

Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val Gly Tyr  
                               30                              35                              40

Thr Ile Pro Cys Cys Arg Asn Glu Xaa Asn Glu Cys Asp Ser Cys Leu  
                               45                              50                              55

Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Xaa Ser Cys Arg Asn  
                               60                              65                              70

Gly Ser Trp Gly Gly Thr Leu  
   75                              80

## (2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 80 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -27..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 7.2  
                            seq SLLFFLLLEGGXT/EQ
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Arg Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu  
    -25                    -20                    -15

Leu Phe Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His  
    -10                    -5                    1                    5

Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu  
            10                    15                    20

Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn  
            25                    30                    35

Cys Ile Cys Ser Glu Xaa Gly Asn Val Leu Cys Ser Arg Val Arg Cys  
            40                    45                    50

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 81 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -19..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 7.2  
                            seq VSIMLLLVTVSDC/AV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val  
                           -15                          -10                          -5

Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys  
                           1                          5                          10

Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg  
           15                          20                          25

Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser  
   30                          35                          40                          45

His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys  
                           50                          55                          60

Leu

## (2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
                                           seq SALLFSLLEAST/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu  
   -20                          -15                          -10

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro  
   -5                          1                          5                          10

Xaa Thr Asn Asn Phe Xaa Asp Xaa Glu Ala Ala Leu Lys Ala His  
           15                          20                          25

## (2) INFORMATION FOR SEQ ID NO: 347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq SALLFSSLCEAST/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu  
-20 -15 -10

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro  
-5 1 5 10

Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln Leu  
15 20 25

Asp Ser Ala Asp Ile Pro Lys Ala Arg Arg Lys Arg Tyr Ile Ser Gln  
30 35 40

Asn Asp Met Ile Ala Ile Leu Asp Tyr His Asn Gln Val Arg Gly Lys  
45 50 55

Val Phe Pro Xaa Ala  
60

## (2) INFORMATION FOR SEQ ID NO: 348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq LLTLVLCVAVAYE/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Asp Pro Asn Gly Gly Cys Cys Thr Leu Leu Thr Leu Val Leu Cys  
-20 -15 -10



Val Ala Val Ala Tyr Glu Arg Gln Glu  
-5 1

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq LFTFSTSLPSSLS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Gly Glu Ile Tyr Phe Gln Val Phe Leu Ser Leu Phe Thr Phe  
-25 -20 -15 -10  
Ser Thr Ser Leu Pro Ser Ser Leu Ser Ser Ser Ser Leu Ser Ser Ser  
-5 1 5  
Asn Gly

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq FLCMLAAIDLALS/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
 -40 -35 -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
 -25 -20 -15 -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met  
 -5 1

## (2) INFORMATION FOR SEQ ID NO: 351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq PWFLAPWCPTQS/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Arg Glu Thr Xaa Pro Leu Pro Lys Pro Leu Lys Asp Thr Ala Pro  
 -40 -35 -30

Ser Ser His Gly Val Gly Ser Asp Ser Pro Ser Ala Thr Arg Pro Trp  
 -25 -20 -15

Phe Leu Ala Pro Trp Cys Pro Gly Thr Gln Ser Asn Arg Ile Cys His  
 -10 -5 1 5

Pro Pro Leu Ser Ser Pro Pro Asp Gln Ala Thr Cys Leu Arg Gly  
 10 15 20

## (2) INFORMATION FOR SEQ ID NO: 352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -60..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7  
 seq VLVVLALRSLGRS/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

```

Met Asp Arg Pro Gly Ser Leu Ser Val Phe Gly Ser Leu Pro Ala Ser
-60 -55 -50 -45

Leu Gly Thr Trp Leu Ser Ser Pro Ala Trp Leu Val Asp Arg Pro Val
 -40 -35 -30

Arg Ser Ala His Pro Ser Ala Asn Ser Thr Gly Val Arg Met Ser Val
 -25 -20 -15

Leu Val Val Leu Ala Leu Arg Ser Leu Gly Arg Ser Cys Ser Leu Ser
 -10 -5 1

Gln Ala Ala Pro Ser Arg Trp Thr Arg Ser Asn Asp Ala Pro Gln Pro
 5 10 15 20

Pro Gly Ser Gln His Ile Phe His Thr Xaa Val Pro Gly
 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 353:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -21..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7  
 seq VILFSYPSCCLC/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

```

Met His Tyr Phe Val Ala Gly Lys Val Ile Leu Leu Phe Ser Tyr Pro
-20 -15 -10

Ser Cys Cys Leu Cys Phe Leu Val Tyr Arg Arg Val Ser Xaa Leu Phe
-5 1 5 10

Lys Cys Phe Glu
 15

```

## (2) INFORMATION FOR SEQ ID NO: 354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq STVVLQVLTQATS/QD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Asp Leu Asn Ser Ala Ser Thr Val Val Leu Gln Val Leu Thr Gln  
                  -15                  -10                  -5  
Ala Thr Ser Gln Asp Thr Ala Val Leu Lys Pro Ala Glu Glu Gln Leu  
                  1                  5                  10  
Lys Gln Trp Glu Thr Gln Pro Gly Phe Tyr Ser Val Leu Leu Asn Ile  
          15                  20                  25  
Phe Thr Asn His Gly  
          30

## (2) INFORMATION FOR SEQ ID NO: 355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq FLCMLAAIDLALS/TS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile .
 -70 -65 -60

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
 -55 -50 -45

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
 -40 -35 -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 -25 -20 -15 -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met
 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 356:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -56...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq PLFFSCSISATHS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```

Met Tyr Arg Leu Ser Leu Ile Ala Gly Pro Gly Ser Tyr Pro Val Leu
 -55 -50 -45

Arg Trp Gly Val Trp Asp Ile Pro Ser Ser Leu Val Gln Val Thr Tyr
 -40 -35 -30 -25

His Gln Pro Asn Leu Thr Thr Asn Leu Asp Leu Pro Leu Phe Phe Ser
 -20 -15 -10

Cys Ser Ile Ser Ala Thr His Ser Cys Val Lys Pro Pro Ser Val Ile
 -5 1 5

Ile Gly Ile Ser Ser Phe Leu Ser Phe Pro Tyr Gln Thr Leu Val
 10 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 357:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq LCFLLLAVAMSFF/GS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu  
                  -20                  -15                  -10

Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu  
                  -5                                  1                                  5

Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly  
          10                                  15                                  20

Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met  
          25                                  30                                  35                                  40

Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe  
                  45                                  50                                  55

Pro Pro Ser Met His Phe Phe Gln Ala Lys Trp  
                  60                                  65

## (2) INFORMATION FOR SEQ ID NO: 358:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq XLXXLLTPPPSYG/HQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```

Met Pro Cys Ser Leu Thr Trp Arg Leu Pro Pro Arg Thr Cys Gln Xaa
-35 -30 -25 -20

Xaa Gly Leu Xaa Lys Ser Xaa Leu Xaa Xaa Leu Leu Thr Pro Pro Pro
 -15 -10 -5

Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser Xaa Gly Ala
 1 5 10

Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys
 15 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq LFLFLTSIAEXCS/TP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Val Xaa Trp Leu Val Leu Phe Ala Leu Gln Ile Tyr Ser Tyr Xaa
-40 -35 -30

Ser Thr Arg Asp Gln Pro Ala Ser Arg Xaa Arg Leu Leu Phe Leu Phe
-25 -20 -15 -10

Leu Thr Ser Ile Ala Glu Xaa Cys Ser Thr Pro Tyr Ser Leu Leu Gly
 -5 1 5

Xaa Val Phe Thr Val Ser Phe Val Ala Leu Gly Val Leu Thr Leu Cys
 10 15 20

Lys Phe Tyr Leu Gln Gly Tyr Arg Ala Phe Met Asn Asp Pro Ala Met
 25 30 35

Asn Arg Gly Gly Ala
 40

```

## (2) INFORMATION FOR SEQ ID NO: 360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LPLLXXXSLPVGA/WL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Ala Arg His Gly Leu Pro Leu Leu Xaa Xaa Xaa Ser Leu Pro Val  
-15 -10 -5  
Gly Ala Trp Leu  
1

## (2) INFORMATION FOR SEQ ID NO: 361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILYILWYCSVCSS/GS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Val His Leu Arg Thr Gly Leu Met Leu Met Ser Ala Asp Arg Leu  
-35 -30 -25  
Arg Thr Leu Tyr Tyr Thr Val Thr Ile Leu Tyr Ile Leu Trp Tyr Cys  
-20 -15 -10  
Ser Val Cys Ser Ser Gly Ser Leu Leu Ser Thr Ser Ile Met Lys Lys  
-5 1 5 10



Arg Met

## (2) INFORMATION FOR SEQ ID NO: 362:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILSTVTALTFARA/LD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu  
-15                      -10                      -5                      1

Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg  
                    5                      10                      15

Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser  
            20                      25                      30

Thr Gln Gln  
            35

## (2) INFORMATION FOR SEQ ID NO: 363:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5  
seq LTFLQXLLISLX/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

```

Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Xaa
 -20 -15 -10

Leu Leu Ile Ser Ser Leu Xaa Arg Glu Tyr Thr Val Ile Asn Glu Ala
 -5 1 5

Arg Lys
 10

```

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq FLLCXSVFTDCKG/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

```

Met Glu Leu Leu Arg Val Cys Ser Phe Phe Leu Leu Cys Xaa Ser Val
 -20 -15 -10

Phe Thr Asp Cys Lys Gly Asp Val Leu Cys Val Lys Met Glu Gln Ser
 -5 1 5 10

Gln Ile Cys Ala

```

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq TWELLPPGQCRA/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Ile Val Arg Pro Arg Leu Asn Leu Thr Trp Phe Leu Leu Leu Pro  
-20 -15 -10

Pro Gly Gln Cys Arg Ala Val Gly Ala Thr Trp Pro Gly  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu Trp Lys  
-15 -10 -5

Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu Lys Cys  
1 5 10

Leu Leu Asp Lys Ala His Val Gly  
15 20

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq CVCAAAXXSQLX/XX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

```

Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Xaa Xaa
-20 -15 -10

Ser Gln Ser Leu Xaa Xaa Xaa Ala Ala Val Ala Ala Ala Gly Gly Arg
-5 1 5 10

Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Xaa Ile
 15 20 25

Ser Gln Tyr Asp Lys Glu Xaa Gly Xaa Trp Asn Lys Phe Arg Asp Asp
 30 35 40

Xaa Tyr
45

```

## (2) INFORMATION FOR SEQ ID NO: 368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu
-20 -15 -10

Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu
-5 1 5 10

Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys Gly

```

15 20 25  
Tyr Ile Phe Ser Leu Ile Ser Pro Gly  
30 35

## (2) INFORMATION FOR SEQ ID NO: 369:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq LWILLGSLSCRTS/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Ala Gln His Leu Trp Ile Leu Leu Gly Ser Leu Ser Cys Arg Thr  
-15 -10 -5  
Ser Asn Arg Arg  
1

## (2) INFORMATION FOR SEQ ID NO: 370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq LYLESFGWTFXLG/KF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Asn Lys Glu Xaa Val Ser Xaa Glu Arg Xaa Ala Gln Val Arg Leu  
                   -25                  -20                  -15

Tyr Leu Phe Ser Gly Phe Trp Thr Phe Xaa Leu Gly Lys Phe Lys Gln  
                   -10                  -5                  1

Gly Glu Xaa Ser Tyr Xaa Xaa Ile Leu Glu Arg Leu Leu Trp Gln Gln  
   5                  10                  15                  20

Gln Tyr Xaa Gly Trp Leu Val Gly Asp Lys Arg  
                   25                  30

## (2) INFORMATION FOR SEQ ID NO: 371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq IVFIFLILLNTAA/QV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Val Leu Trp Arg Ala Lys Ile Xaa Arg Asn Val Pro Val Thr Leu  
                   -50                  -45                  -40

Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys  
                   -35                  -30                  -25

Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile  
                   -20                  -15                  -10

Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp  
   -5                  1                  5                  10

Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn  
                   15                  20                  25

## (2) INFORMATION FOR SEQ ID NO: 372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq FTSVLWLTPSQP/NT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Leu Leu Xaa Phe Phe Thr Ser Val Leu Trp Leu Thr Ser Pro Ser  
-15 -10 -5  
Gln Pro Asn Thr Cys Pro Ser Ser Leu Leu Cys Thr Tyr Pro Asn Leu  
1 5 10  
Asn Pro Pro Trp  
15

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq IILGCLALFLLLQ/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Leu Gly Cys Leu Ala  
-20 -15 -10  
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Trp  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq TWLGLLSFQNLHC/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly  
-45 -40 -35  
Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser  
-30 -25 -20  
Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe  
-15 -10 -5 1  
Pro Asp Leu Pro Gly  
5

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq NTLFLHLSGLSAA/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Thr Trp Val Arg His Ala Pro Gly Lys Ser Leu Glu Trp Val Ala  
-55 -50 -45  
Thr Val Thr Asp Gly Gly Asp Lys Thr Phe Tyr Ala Ala Ser Val Lys



-40                      -35                      -30                      -25  
Gly Arg Phe Asn Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu  
                         -20                      -15                      -10  
His Leu Ser Gly Leu Ser Ala Ala Asp Thr Gly Trp Trp Gly Ile  
                         -5                      1                      5

## (2) INFORMATION FOR SEQ ID NO: 376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LTSFFSLTANCQS/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

Met Leu Thr Ser Phe Phe Ser Leu Thr Ala Asn Cys Gln Ser Ala Gly  
                         -10                      -5                      1  
Thr Ile Ser Phe Ala Ala Phe Ser Leu Met Pro Gly  
                         5                      10

## (2) INFORMATION FOR SEQ ID NO: 377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LTPLFFMXPTGFS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Xaa Pro Thr Gly  
-15 -10 -5  
Phe Ser Ser Pro Ser Pro Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq HSLFLSLLGLCPS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Asp Asp Asp Tyr Glu Ala Tyr His Ser Leu Phe Leu Ser Leu Leu  
-20 -15 -10  
Gly Leu Cys Pro Ser Lys Thr Pro Ile Asn Glu Asn Ala Pro Val Phe  
-5 1 5 10  
Asp Pro Glu Pro Val  
15

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq WLWVLLLGHMVVS/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Glu Trp Gly Lys Gln Trp Leu Val Trp Leu Leu Leu Gly His Met  
-15 -10 -5  
Val Val Ser Gln Met Ala Thr Leu Leu Ala Arg Lys His Arg Pro Trp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -39..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq LTQGVWLWILVIQA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Arg Arg Gly Lys Arg Leu Leu Glu Ser Gln Ser Ser Ser Pro Lys  
-35 -30 -25  
Ala Cys Leu Gln Leu Gly Phe Glu Thr Glu Leu Thr Gln Gly Val Leu  
-20 -15 -10  
Trp Ile Leu Val Ile Gln Ala Val Pro Val Pro Ser Leu Thr Lys Thr  
-5 1 5  
Lys  
10

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ALLESVVWLPCHG/RG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Val Ala Ala Thr Glu Ala Ala Leu Leu Glu Ser Val Val Trp Leu  
-20 -15 -10 -5

Pro Cys His Gly Arg Gly Gly Ser  
1

## (2) INFORMATION FOR SEQ ID NO: 382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq VSLPLLSSWGSTA/WT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Ser Trp Asn Pro Ser Val Ser Leu Pro Leu Leu Ser Ser Trp Gly  
-15 -10 -5

Ser Thr Ala Trp Thr Leu  
1

## (2) INFORMATION FOR SEQ ID NO: 383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LILLSLHLERRWT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Lys Arg Ile Gln Gly Ile Leu Phe Leu Ile Leu Leu Ser Leu His
 -20 -15 -10

Leu Glu Arg Arg Trp Thr Ser Pro Ser Asp His Ser Leu Leu Leu Gly
 -5 1 5 10

Gly Asn Ser Leu Ala Gln His Ala Glu Ser Val Val Arg Gln Gly
 15 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 384:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -35..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq LLTFGLEVCLAAG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

```

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
-35 -30 -25 -20

Gln Leu Xaa Leu Xaa Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 -15 -10 -5

Ala Ala Gly Ser Pro Met Cys Arg Leu Cys Cys Trp Lys Trp
 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 385:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq PFALVTSCSSVFS/GD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Ala Ala Gly Val Pro Phe Ala Leu Val Thr Ser Cys Ser Ser Val  
          -15                          -10                          -5

Phe Ser Gly Asp Gln Leu Val Gln His Ile Leu Gly Thr Glu Asp Leu  
          1                                          5                          10

Ile Val Glu Val Thr Ser Asn Asp Ala Val Arg Phe Tyr Pro Trp Thr  
15                                  20                                  25                                  30

Ile Asp Asn Lys Tyr Tyr Ser Ala Asp Ile Asn Leu Cys Val Val Pro  
                                  35                                  40                                  45

Asn Lys Phe Leu Val Thr Ala Glu Ile Ala Glu Ser Val Gln Ala Phe  
                                  50                                  55                                  60

Val Val Tyr Phe Asp Xaa Thr Gln Xaa Ser Gly Leu Asp Ser Val Ser  
          65                                  70                                  75

Ser Trp Leu Pro Leu Ala Lys Ala Trp Leu Pro Glu Val Met Ile Leu  
          80                                  85                                  90

Val Cys Asp Arg Val Ser Glu Asp Gly Ile  
95                                  100

## (2) INFORMATION FOR SEQ ID NO: 386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq TVFLXFCFPRCHS/DS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Thr Val Phe Leu Xaa Phe Cys Phe Pro Arg Cys His Ser Asp Ser  
                   -10                  -5                  1

His Xaa Xaa Gln Gln Ser Ala  
                   5

## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq ILLEVFVWNLQG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Met Xaa Pro Asn Asn Phe Trp Gln Lys Leu Gly Arg Lys Lys Pro Arg  
                   -45                  -40                  -35

Ile Phe Thr Cys Thr Gln Ser Ser Thr Gly Glu Ala Ala Val Lys Ala  
                   -30                  -25                  -20

Glu Asn Leu Ile Leu Leu Glu Val Phe Val Trp Asn Gly Leu Gln Gly  
                   -15                  -10                  -5

Leu Pro Ser Glu Leu Ser Asp Thr Ser Gly Ser Ser Lys Lys Leu Gly  
   1                  5                  10                  15

Ser Leu Val Gly Trp Trp Arg Thr Leu Lys Met Ala Pro Ala Cys Leu  
                   20                  25                  30

Trp Ser Met Trp Glu Ser Pro Pro Arg  
                   35                  40

## (2) INFORMATION FOR SEQ ID NO: 388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq ALYIMCVPHSVWG/CA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Phe Arg Ser Asp Arg Met Trp Xaa Cys His Trp Lys Trp Lys Pro  
-35 -30 -25

Ser Pro Leu Leu Phe Leu Phe Ala Leu Tyr Ile Met Cys Val Pro His  
-20 -15 -10 -5

Ser Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro Ser  
1 5 10

Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser Gln  
15 20 25

Ala Cys Met Trp Thr Leu Arg Asp Pro  
30 35

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq LVALSSELPFLGA/GV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:



```

Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys Asn Leu Lys Phe Val
-30 -25 -20

Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala Gly
-15 -10 -5 1

Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
 5 10 15

Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
 20 25 30

Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
 35 40 45

Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Gln
 50 55 60

```

## (2) INFORMATION FOR SEQ ID NO: 390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq IIPLLLLLSACN/VH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

```

Met Ile Ile Pro Leu Leu Leu Leu Arg Ser Ala Cys Asn Val His
 -10 -5 1

Leu Pro His Gln Thr Ala Ser Pro Ala Ser Leu Ser Pro Gln Gly Leu
 5 10 15

Ala Trp Gly Leu Leu His Gly Gly Cys Ser Val Thr Val Arg
 20 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3  
seq VLLLSXNLLNLIQ/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Xaa Ser Pro Leu Pro Val Leu Leu Leu Ser Xaa Asn Leu Asn Leu  
-15 -10 -5

Ile Ile Gln Ser Ser  
1

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2  
seq LLTFLVFTXKLSS/LN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Leu Met Cys Lys Met Leu Lys Ser Gln Lys Asn Cys Gln Glu Asn  
-45 -40 -35

Xaa Xaa Ile Lys Ile Ile Leu Phe Leu Lys Pro Met Cys Ser Pro Gln  
-30 -25 -20 -15

Tyr Leu Leu Thr Phe Leu Val Phe Thr Xaa Lys Leu Ser Ser Leu Asn  
-10 -5 1

Ile Xaa Lys Phe His  
5

## (2) INFORMATION FOR SEQ ID NO: 393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq IIVILHCAASIIS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Lys Lys Lys Ser Ser Pro Asn Gln Tyr Leu His Ser Ser Leu His
 -50 -45 -40

Xaa Ile Arg Leu Phe Ser Phe Leu His Phe Ser Glu Glu Gly Val Leu
 -35 -30 -25

Leu Leu Ala Ile Asp Leu Lys Ile Ile Val Ile Leu His Cys Ala Ala
 -20 -15 -10 -5

Ser Ile Ile Ser Cys Pro Ser
 1

```

## (2) INFORMATION FOR SEQ ID NO: 394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq ATSVSLEAQSCFA/WP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Phe Ser Cys Phe Phe Ser Thr Ser Leu Ala Thr Ser Val Ser Leu  
                   -20                  -15                  -10

Glu Ala Gln Ser Cys Phe Ala Trp Pro Leu Ile Val Ser Phe Pro Gln  
                   -5                                  1                                  5

Gly Ser Leu Leu Ser Pro Phe Leu Leu Met Ser Tyr Asn Leu Ser His  
   10                                  15                                  20                                  25

Leu Ile Tyr Ser Gly Glu Leu Asn Gly Arg Leu Tyr Ala Glu Asn Ser  
                                   30                                  35                                  40

Gln Ile Cys Ile Cys Ser Pro Ala Gly  
                   45                                  50

## (2) INFORMATION FOR SEQ ID NO: 395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -50..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
                                   seq RTALILAVCCGSA/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met His-His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys  
   -50                  -45                  -40                  -35

Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala  
                   -30                  -25                  -20

Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly  
                   -15                  -10                  -5

Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser  
       1                                  5                                  10

Ser Gln Asp Leu Ser Gly Gln Thr Ala Pro Gly  
   15                                  20                                  25

## (2) INFORMATION FOR SEQ ID NO: 396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq IYFFACFQALTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Gln Ala Leu Thr Ser  
-15 -10 -5

Ser Ser Pro Pro Gln  
1

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Xaa Phe Ser Ser Ser  
-30 -25 -20

Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg  
-15 -10 -5 1

Ile Phe Lys Ile Ile Val Ile Gly Asp Xaa Asn Val Gly Lys Thr Cys  
5 10 15

Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg Thr Glu Ala

20                                  25                                  30

Thr Ile Gly Val Asp Phe Arg Glu Arg Ala Val Glu Ile Asp Gly Glu  
      35                                  40                                  45

Arg Ile Lys Ile Gln Leu Trp Asp Thr Ala  
   50                                  55

(2) INFORMATION FOR SEQ ID NO: 398:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 61 amino acids
      (B) TYPE: AMINO ACID
      (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -31..-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 5.1
                               seq VSGASGFLPPARS/RI
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Ser Phe Ser Ser Ser
-30 -25 -20

Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg
-15 -10 -5 1

Ile Phe Lys Ile Ile Val Ile Gly Asp Ser Asn Val Xaa Lys Thr Cys
5 10 15

-

Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -27..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5
 seq HLSLILLKPLCLP/NN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Leu Val Leu Gly Ser Pro Leu Leu Gly Pro Leu Leu Trp His Leu
 -25 -20 -15
 Ser Leu Ile Leu Leu Lys Pro Leu Cys Leu Pro Asn Asn Leu Pro Leu
 -10 -5 1 5
 Ala Leu Gly Arg Cys Leu Cys Leu His Ser
 10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -55..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5
 seq VLFMTTAVDLVIT/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met His Leu Leu Asp Leu Glu Ser Met Gly Lys Ser Ser Asp Gly Lys
 -55 -50 -45 -40
 Ser Tyr Val Ile Thr Gly Ser Trp Asn Pro Lys Ser Pro His Phe Gln
 -35 -30 -25
 Val Val Asn Glu Glu Thr Pro Lys Asp Lys Val Leu Phe Met Thr Thr
 -20 -15 -10
 Ala Val Asp Leu Val Ile Thr Glu Val Gln Glu Pro Val Arg Phe Leu
 -5 1 5
 Leu Glu Thr Lys Val Arg Val Cys Ser Pro Asn Glu Arg Leu Phe Trp
 10 15 20 25
 Pro Ala

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VLFVFSSIPLTFL/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

```

Met Glu Asn Leu Lys Asp Phe Tyr Val Leu Phe Val Phe Ser Ser Ile
-20                               -15                -10

Pro Leu Thr Phe Leu Phe Gln Lys Leu Pro Phe Val Trp Ile Xaa Glu
-5                               1                5                10

Glu Thr Leu Glu Thr Trp Tyr Leu Lys Ser Trp
15                               20

```

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LSIFSLVLPVCRM/HR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

```

Met Pro Gln Tyr Cys Leu Ser Ile Phe Ser Leu Val Leu Pro Val Cys
-15                               -10                -5

```


Arg Met His Arg

1

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LLAFGTSCSVVLY/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn
 -40 -35 -30

Arg Val Arg Gly Val Leu Asn Trp Ser Ser Gly Pro Arg Gly Leu Leu
 -25 -20 -15

Ala Phe Gly Thr Ser Cys Ser Val Val Leu Tyr Asp Pro Leu Gly Cys
 -10 -5 1 5

Cys Tyr Gln Leu Glu Trp Ser His Arg Pro Phe Arg
 10 15

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LSWLITWFGHXL/DF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

```
Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His Asp Phe Met Gln  
          -35                      -30                -25
```

```
Ser Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp Leu Ile Thr Trp  
      -20                        -15                -10
```

```
Phe Gly His Xaa Leu Ser Asp Phe Arg His Val Val Arg Leu Tyr Asp  
    -5                          1              5                10
```

```
Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr Phe Ala Ala Val  
           15                     20                25
```

```
Ile Val Leu Tyr Arg Glu Gln  
        30
```

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -49..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.7
seq GLCVLVPCXSXX/WR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met	Glu	Thr	Xaa	Cys	Pro	Cys	Cys	Cys	Cys	Pro	Cys	Xaa	Gly	Xaa	Gly	-45	-40	-35
Ser	Leu	Xaa	Xaa	Lys	Pro	Val	Tyr	Glu	Leu	Gln	Val	Gln	Lys	Ser	Val	-30	-25	-20
Thr	Val	Gln	Glu	Gly	Leu	Cys	Val	Leu	Val	Pro	Cys	Ser	Xaa	Ser	Xaa	-15	-10	-5
Xaa	Trp	Arg	Ser	Trp	Tyr	Ser	Ser	Pro	Pro	Leu	Tyr	Val	Tyr	Trp	Phe	1	5	10
Arg	Asp	Gly	Glu	Ile	Pro	Tyr	Tyr	Ala	Glu	Val	Val	Ala	Thr	Asn	Asn	20	25	30
Pro	Asp	Arg	Arg	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Pro	Ile	Pro	Pro	Pro		35	40	45

Trp Gly Cys Pro Glu Glu Glu Leu
50 55

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq IYFFACFXXLTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Xaa Xaa Leu Thr Ser
-15 -10 -5
Ser Ser Pro Pro His Pro Cys Pro Lys Cys Trp Pro Ser Ser Gly Ser
1 5 10 15
Ile Pro Leu

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq VLKCLSFSXPSLP/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Met Gly Arg Gly Glu Arg Arg His Tyr Trp Gly Pro Lys Leu Val Leu
-25 -20 -15

Lys Cys Leu Ser Phe Ser Xaa Pro Ser Leu Pro Gly Phe Leu Trp Ser
-10 -5 1 5

Leu

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -52..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LLAKALHLLKSSC/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser
-50 -45 -40

Phe Arg Val Ser Glu Leu Gln Val Leu Leu Gly Phe Ala Gly Arg Asn
-35 -30 -25

Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu
-20 - -15 -10 -5

Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr
1 5 10

Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu
15 20 25

Lys

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -69..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LGPSLSSLPSALS/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

Met His His Arg Met Asn Glu Met Asn Leu Ser Pro Val Gly Met Glu
 -65 -60 -55
Gln Leu Thr Ser Ser Ser Val Ser Asn Ala Leu Pro Val Ser Gly Ser
 -50 -45 -40
His Leu Gly Leu Ala Ala Ser Pro Thr His Ser Ala Ile Pro Ala Pro
 -35 -30 -25
Gly Leu Pro Val Ala Ile Pro Asn Leu Gly Pro Ser Leu Ser Ser Leu
 -20 -15 -10
Pro Ser Ala Leu Ser Leu Met Leu Pro Met Gly Xaa Gly Asp Arg Gly
 -5 1 5 10
Val Met Cys Gly Leu
 15

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq IWNLFSLFSTSTT/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Leu His Ser Asp Asn Ile Trp Asn Leu Phe Ser Leu Phe Ser Thr
 -15 -10 -5

Ser Thr Thr Leu Pro Arg
1

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq FHSAAGWSGGGQA/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Gln Pro Ala Ser Pro Pro Ala Arg Trp Ser Phe His Ser Ala Ala
-20 -15 -10
Gly Trp Ser Gly Gly Gly Gln Ala Cys Gly Gly His Ser Cys Asp Gln
-5 1 5
Val Leu Ala Val Ile Glu Leu Leu Asn Pro Leu Arg
10 15 20

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LLAGSISHMFSQA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Cys Phe Ser Phe Leu Leu Ala Gly Ser Ile Ser His Met Phe Ser
-15 -10 -5
Gln Ala Leu Pro Leu His Ser Pro Gly Leu Pro Thr Thr Asn Arg Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq SILFHCSVCLFLC/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Tyr Gly Phe Ile Ile Gly Leu Ser Ile Leu Phe His Cys Ser Val
-20 -15 -10
Cys Leu Phe Leu Cys Gln Tyr His Ala Trp
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq SLLGCKLAININT/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ser Phe Gly Xaa Ile Leu Thr Phe Arg Val Ser Leu Leu Gly Cys
 -20 -15 -10
 Xaa Leu Ala Ile Asn Ile Asn Thr Phe Pro Ser Asn Asn His Leu
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LGRLCAGSSGVXG/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
 -20 -15 -10
 Ser Ser Gly Val Xaa Gly Ala Arg Ala Xaa Leu Ser Arg Ser Trp Gln
 -5 1 5 10
 Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg Glu Val Asp
 15 20 25
 Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val Gln Gly Cys
 30 35 40
 Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys Leu Glu Thr
 45 50 55
 Thr Ala Gln Arg Val Pro
 60

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LVSIFFFWVTNA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Phe Asn Thr Ile Tyr Leu Val Ile Ser Leu Val Ser Ile Phe Phe
-20 -15 -10

Phe Trp Glu Val Thr Asn Ala Phe Leu Lys Ala Arg Arg Trp
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq SLPLTTGSSWSLS/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Leu Pro Pro Lys Gly Cys Gly Ser Leu Pro Leu Thr Thr Gly
-20 -15 -10

Ser Ser Trp Ser Leu Ser Ser Gln Ile Gly Ser Pro Ala Ile Ser Asn
-5 1 5 10

Pro Arg

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3
seq FLSWASFLAPLLR/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Phe Val Phe Leu Ser Trp Ala Ser Phe Leu Ala Pro Leu Leu Arg
-15 -10 -5

Ser Pro Phe Leu His Cys Leu Met Gly Met Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3
seq LLSCSPLXPLGKS/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Xaa Met Lys Ser Ala Asn Lys Ile Thr Leu Leu Xaa His His Leu
-25 -20 -15

Leu Ser Cys Ser Pro Leu Xaa Pro Leu Gly Lys Ser Gly Phe Ser Ser
-10 -5 1

Cys Gln Arg Leu Gly Lys Arg Ala Leu Val Phe Pro Ile Xaa Lys Xaa
5 10 15 20

Ile Ile Thr

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SFLLLFIVIPQTP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Cys Asn Tyr Asn Ile Tyr Val Leu Tyr Asn Ile Gly Tyr Leu Tyr
-30 -25 -20

His Pro Lys Ser Phe Leu Leu Phe Ile Val Ile Pro Gln Thr Pro
-15 -10 -5

Arg Pro
1

(2) INFORMATION FOR SEQ ID NO: 421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq PLLAAPLLRSLLP/RX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Ala Val Ala Met Val Lys Leu Cys Glu Arg Ala Gly Leu Pro Leu
-25 -20 -15

Leu Ala Ala Pro Leu Leu Arg Ser Leu Leu Pro Arg Xaa Pro Gln Pro
 -10 -5 1 5
 Gly Pro Ala Gln Pro Arg Ser Val Gln Gly Gln Arg Cys Pro Ala Arg
 10 15 20
 His Pro Pro Gly Asn Leu Val Cys Glu Arg Gly Ala Xaa Val Asn Gly
 25 30 35
 Val Thr Ala Gly Ala Xaa Gly Xaa Leu Arg Gly Leu His Arg Gly Xaa
 40 45 50
 Arg Ala Leu Gly Cys Ser Ala His Arg Pro Xaa His Ser Ala Arg Val
 55 60 65
 Arg Pro Pro Ala
 70

(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -122..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq DVLLGLLKDVLLA/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Leu Asn Val Val Arg Ala Leu Arg Xaa Pro Gln Trp Cys Ala Glu
 -120 -115 -110
 Tyr Cys Leu Ser Ile His Tyr Gln His Gly Gly Val Ile Cys Thr Gln
 -105 -100 -95
 Val His Lys Gln Thr Val Val Gln Leu Ala Leu Arg Val Ala Asp Glu
 -90 -85 -80 -75
 Met Asp Val Asn Ile Gly His Glu Val Gly Tyr Val Ile Pro Phe Glu
 -70 -65 -60
 Asn Cys Cys Thr Asn Glu Thr Ile Leu Arg Tyr Cys Thr Asp Asp Met
 -55 -50 -45
 Leu Gln Arg Glu Met Met Ser Asn Pro Phe Leu Gly Ser Tyr Gly Val
 -40 -35 -30

Ile Ile Leu Asp Asp Ile His Glu Arg Ser Ile Ala Thr Asp Val Leu
-25 -20 -15
Leu Gly Leu Leu Lys Asp Val Leu Leu Ala Arg Pro Glu Leu Lys
-10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq AGLCIGSTSYVHG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met His Ala Gly Leu Glu Arg Xaa Ser Xaa Gln Lys Ala Leu Ala Gly
-25 -20 -15
Leu Cys Ile Gly Ser Thr Ser Tyr Val His Gly Asp Ile Leu Arg Thr
-10 -5 1 5
Glu Arg

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LLGSLSLWRWSAM/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

```

Met Leu Asn Gly Pro Phe Gln His Arg Asn Ser Arg Ile Met Thr His
-35          *   -30          -25          -20

Arg Ser Ala Glu Lys Thr Leu Leu Gly Ser Leu Ser Leu Trp Arg Trp
          -15          -10          -5

Ser Ala Met Glu Pro Thr Asp Arg Cys Thr Arg Val Gly
          1          5          10

```

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

```

Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg
          -40          -35          -30

Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile
          -25          -20          -15

Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn
          -10          -5          1

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu
          5          10          15          20

Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser
          25          30          35

Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn
          40          45          50

Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu
          55          60          65

Pro His Cys Ile Ile Ile Asn Leu Ser Thr
          70          75

```

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FSLALSMLKGTG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Pro Gln Lys Gly Leu Gly Leu Leu Gly Ile Leu Ser Gly Asp Phe
-25 -20 -15

Ser Leu Leu Ala Leu Ser Met Leu Lys Gly Thr Gly Lys Val Gly Gly
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq AALCGISLSQLFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln Pro Leu
-55 -50 -45 -40

Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
-35 -30 -25

Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
 -20 -15 -10
 Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr
 -5 1 5
 Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu Ala Val
 10 15 20 25
 Leu Pro Thr Met Thr Ala
 30

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LLLSPWVTVPVWS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Leu Cys Phe Gly Asp Leu Leu Leu Ser Pro Trp Val Thr Val Pro
 -15 -10 -5
 Val Trp Ser Ser Ser Pro Trp
 1

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -27..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq LIYFLGLAADTYF/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Gln Glu Asn Ala His Asn Leu Arg Leu Phe Lys Cys Leu Leu Ile
 -25 -20 -15
 Tyr Phe Leu Gly Leu Ala Ala Asp Thr Tyr Phe Arg Ser Lys Arg Lys
 -10 -5 1 5
 Pro Val Ser Phe Val Val Thr Val Xaa Xaa Gly Xaa Tyr Ala Thr Gly
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -59..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq SVATALFPPLCIS/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met His Thr Cys Ser Leu Pro Cys Leu Leu Phe Ala Gln Leu Leu Glu
 -55 -50 -45
 Phe Cys Ser Phe Pro Pro Asp Val Pro His Asn Cys Ala Pro Ile Val
 -40 -35 -30
 Ser Val Arg Pro Pro Asn Ile Val Ala Ala Phe Glu Gly Cys Ser Val
 -25 -20 -15
 Ala Thr Ala Leu Phe Pro Pro Leu Cys Ile Ser Thr Gly Asn Glu
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4
seq PLLGVLFFQGVYI/VF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Gln Gln Arg Gly Ala Ala Gly Ser Arg Gly Cys Ala Leu Phe Pro
-25 -20 -15
Leu Leu Gly Val Leu Phe Phe Gln Gly Val Tyr Ile Val Phe Ser Leu
-10 -5 1
Glu Ile Arg Ala Asp Ala His Val Arg Gly Tyr Val Gly Glu Lys Ile
5 10 15 20
Lys Leu Lys Cys Thr Phe Lys Ser Thr Ser Asp Val Thr Asp Lys Leu
25 30 35
Thr Ile Asp Trp Thr Tyr Arg Pro Pro Ser Ser Ser His Thr Val Ser
40 45 50
Ile Xaa His Tyr Gln Ser Phe Gln Tyr Pro Thr Thr Ala Gly Thr Phe
55 60 65

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -39..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq LILNRS LPTASSS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

```

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala
-20              -15              -10              -5

Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Tyr Ile Glu Lys Glu
              1              5              10

Ala Asn Lys Thr Tyr Asn Cys Glu Asn Leu Gly Leu Ser Glu Ile Pro
              15              20              25

Asp Thr Leu Pro Asn Thr Thr Glu Phe Leu Glu Phe Ser Phe Asn Phe
              30              35              40

Leu Pro Thr Ile His Asn Arg Thr Ser Ser Arg
45              50              55

```

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -96..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq IMNLTVMMLDTAXG/KX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

Met Glu Val Ala Ala Asn Cys Ser Leu Arg Val Lys Arg Pro Leu Leu
-95 -90 -85

Asp Pro Arg Phe Glu Gly Tyr Lys Xaa Ser Leu Glu Pro Leu Pro Cys
-80 -75 -70 -65

Tyr Gln Leu Glu Leu Asp Ala Ala Val Ala Xaa Val Lys Leu Arg Asp
-60 -55 -50

Asp Gln Tyr Thr Leu Glu His Met His Ala Phe Gly Met Tyr Asn Tyr
-45 -40 -35

Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr Ile Asp Thr
-30 -25 -20

Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr Ala Xaa Gly
-15 -10 -5

Lys Xaa Arg Glu Val Phe Arg Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq VLAIGLLHIVLLS/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

```

Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg Val
      -35                      -30                      -25
Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
      -20                      -15                      -10
Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
      -5                      1                      5
Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
      10                      15                      20                      25
His Thr Val Lys Gly Xaa Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
      30                      35                      40
Arg Leu Leu Xaa His Xaa Xaa Ala Asp Gly Leu Trp Gly Pro Val
      45                      50                      55

```

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq SWWTLSSSPSFM/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```

Met Glu Asn Phe Asn Met Tyr Lys Asn Lys Ser Trp Trp Thr Leu Leu
      -20                      -15                      -10
Ser Ser Ser Pro Ser Phe Met Ile Ser Phe Val Ser Ser Val Leu Pro
      -5                      1                      5
Val Leu Leu Thr Ile Ser Arg Phe Ile Leu Lys Gln Ile Pro Asp Gln
      10                      15                      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq VLAIGLLHIVLLS/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

```

Met Asn Val Gly Thr Xaa His Ser Glu Val Asn Pro Asn Thr Arg Val
      -35                      -30                      -25

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
      -20                      -15                      -10

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
      -5                      1                      5

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
      10                      15                      20                      25

Tyr Thr Val Lys Gly Thr
      30

```

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq AAASAVSVLLVAA/ER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Ala Ala Ala Ser Ala Val Ser Val Leu Leu Val Ala Ala Glu Arg
 -10 -5 1

Asn Arg Trp His Arg Leu Pro Ser Leu Leu Leu Pro Pro Arg Thr Trp
 5 10 15

Val Trp Arg Gln Arg Thr Met Lys Tyr Thr Thr Ala Thr Gly Arg Asn
 20 25 30

Met
 35

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
 seq SGSGLSWARLSQS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Ala Tyr Ser Lys Ala Ser Gly Ser Pro Val Leu Ser Gln Ala Val
 -40 -35 -30

Pro Gly Glu Asn Ala Ser His Arg Arg Gly Ser Ala Asp Leu Gly Ser
 -25 -20 -15

Gly Ser Gly Leu Ser Trp Ala Arg Leu Ser Gln Ser Arg Ser Glu Ile
 -10 -5 1

His Ser Ala Gly Pro Pro His Leu Gly Gly Arg Thr Asn Gly Pro Glu
 5 10 15 20

Phe Pro Ala Leu Ser Tyr Ser Ser Gln Leu Leu Ser Leu Ala Gln Leu
 25 30 35

Arg Gly Arg Gly Ile Thr Glu Val Ser Glu Lys Ser Pro Leu Ile
 40 45 50

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RPVLLHLHQTAHA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp
-35 -30 -25

Thr Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His
-20 -15 -10

Gln Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His
-5 1 5 10

Thr Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala
15 20 25

Ile Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile
30 35 40

His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Gln
45 50 55

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7
seq IPCAHMLVCPTIG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```

Met Ile Ile Cys Tyr Asp Ile Pro Cys Ala His Met Leu Val Cys Pro
      -15              -10              -5
Thr Ile Gly Asp Ile Lys Phe Asp His Leu Met Lys Trp Tyr Pro Ser
      1              5              10
Asp Phe Ser Thr Glu Arg Leu
      15              20

```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```

Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala Ala
      -15              -10              -5
Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln Met
      1              5              10
Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro Gln
      15              20              25
Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val Glu
      30              35              40              45
Lys Asn Lys Tyr Asp Ala
      50

```

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -65..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq QLEGLNWLRFWSA/QG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Gly Glu Asp Pro Xaa Gln Pro Arg Lys Tyr Lys Lys Xaa Lys Xaa
-65 -60 -55 -50
Glu Leu Gln Gly Asp Xaa Pro Pro Ser Ser Pro Thr Asn Asp Pro Thr
-45 -40 -35
Val Lys Tyr Glu Thr Gln Pro Arg Phe Ile Thr Ala Thr Gly Gly Thr
-30 -25 -20
Leu His Met Tyr Gln Leu Glu Gly Leu Asn Trp Leu Arg Phe Ser Trp
-15 -10 -5
Ala Gln Gly Thr Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq LLGCLQCCWLQSG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Phe Tyr Val Ala Met Thr Lys Thr His Lys Arg Ile Arg Ser Leu
-40 -35 -30

Cys Asn Ile His His Gly Leu Phe Gln Phe Thr Gln Gln Leu Leu Gly
 -25 -20 -15
 Cys Leu Gln Cys Cys Trp Leu Gln Ser Gly Arg Ala Pro Ala Thr Tyr
 -10 -5 1 5
 Tyr Leu Val Glu Ser Ile Glu Lys Ser Ala His Gly Ser Val Leu Xaa
 10 15 20
 Thr Tyr Asp Gln Thr Gln Thr Arg Ile Gly Arg
 25 30

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq XTCASXNPSQCLA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Val Ser Pro Lys Asp Leu Pro Leu Val Leu Leu Gln Asp Ile Lys
 -60 -55 -50 -45
 Val Pro Ser Ser Met Thr Gly Ser His Ala Gly Asn Pro His Ile Glu
 -40 -35 -30
 Arg Asn Asp Leu Pro Arg His Gly Ser Pro Gln Phe Phe Thr Gly Xaa
 -25 -20 -15
 Thr Cys Ala Ser Xaa Asn Pro Ser Gln Cys Leu Ala Ala Phe
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FXSLFCLYFSCFL/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

```

Met Glu Phe Xaa Ser Leu Phe Cys Leu Tyr Phe Ser Cys Phe Leu His
-15                -10                -5                1
Ile Ile Tyr Phe Xaa Ser Cys Phe Leu Tyr
      5                10

```

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -45..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq ALLELIDSPECLS/KC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

```

Met Ala Leu His Phe Gln Ser Leu Ala Glu Leu Glu Xaa Leu Cys Thr
-45                -40                -35                -30
His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala Glu Lys
      -25                -20                -15
Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys Cys Gln
      -10                -5                1
Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu Ala Ala
      5                10                15
Thr Xaa
20

```

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LLLLLITPSPSPL/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

```

Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
   -25                      -20                      -15

Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
  -10                      -5                      1                      5

Leu Ser Leu Arg Ser Ala Met Ser
                   10

```

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq AVSSLIAVGTSHG/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

```

Met Arg His Ser Leu Leu Lys Gly Ile Ser Ala Gln Ile Val Ser Ala
  -40                      -35                      -30

```

Ala Asp Lys Val Asp Ala Gly Leu Pro Thr Ala Ile Ala Val Ser Ser
-25 -20 -15 -10

Leu Ile Ala Val Gly Thr Ser His Gly Leu Ala Gly
 -5 1

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LSCFIFFYISSLC/CF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Thr Leu Ser Cys Phe Ile Phe Phe Tyr Ile Ser Ser Leu Cys Cys
-15 -10 -5 1

Phe Leu Ser Tyr Pro Thr Arg
 5

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LCFLLP HHRLQEA/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
-15 -10 -5 1
Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
5 10 15
Arg Arg Glu Lys Thr Asn Lys Trp Glu Lys Arg Lys Gly Ser Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq FSLFALNMPLGFC/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Phe Ser Leu Phe Ala Leu Asn Met Pro Leu Gly Phe Cys Val Tyr
-10 -5 1
Val Ile Phe Lys Ile His Asp Trp
5 10

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5

seq SVWGVLPFPACSA/DL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Ala Ser Ser Pro Gly Val Ala Met His Ser Leu Trp Ala Thr Ile
 -30 -25 -20
 His Thr Ser Val Trp Gly Val Leu Pro Pro Pro Ala Cys Ser Ala Asp
 -15 -10 -5 1
 Leu Leu Phe Ser Asn Ala Cys Leu Leu Pro His Glu Ile His Leu
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LPRLLSLSQHSSES/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Ser Gln Glu Gly Ala Val Pro Ala Ser Ala Val Pro Leu Glu Glu
 -45 -40 -35 -30
 Leu Ser Ser Trp Pro Glu Glu Leu Cys Arg Arg Glu Leu Pro Ser Val
 -25 -20 -15
 Leu Pro Arg Leu Leu Ser Leu Ser Gln His Ser Glu Ser Trp Ile Glu
 -10 -5 1
 His Ile Gln Ile Leu Lys Ile Ile Val Glu Met Phe Leu Pro His Met
 5 10 15
 Asn His Leu Thr Leu Glu Gln Thr Phe Phe Ser Gln Val Leu Pro Lys
 20 25 30 35
 Thr Val Lys Leu Phe Asp
 40

(2) INFORMATION FOR SEQ ID NO: 455:

Gln Ala Cys Pro Glu Pro Cys Asp Cys Gly Glu Lys Tyr Gly Phe Gln
1 5 10

Ile Ala Asp Cys Ala Tyr Arg Asp Leu Glu Ser Val Pro Pro Gly Phe
 15 20 25 30
 Pro Ala Asn Val Thr Thr Leu Ser Leu Ser Ala Asn Arg Leu Pro Gly
 35 40 45
 Leu Pro Glu Gly Ala Phe Arg Glu Val Pro Leu Leu Gln Ser Leu Trp
 50 55 60
 Leu Ala His Asn Glu
 65

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.6
seq LLLALCATGAQG/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu Cys Ala Thr Gly Ala
 -15 -10 -5
 Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys Arg Cys Phe Ile
 1 5 10
 Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn Tyr Arg Thr Gln
 15 20 25 30
 Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser Thr Pro Gly Leu
 35 40 45
 Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys Val Val Leu Ser
 50 55 60
 Arg Gln Tyr Gly Ser Glu Gly Arg Phe Thr Phe Thr Ser His Xaa Xaa
 65 70 75
 Gly Asp His Gln Ile Cys Leu His Cys Gly
 80 85

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.7
seq ILFLLSWGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
-20 -15 -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
-5 1 5 10

Arg Leu Ala Ala Leu Glu Glu Arg
15

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq LLLLCPLSRGCCP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ser Cys Arg Glu Leu Thr His Arg Pro Cys Ser Pro His Leu Leu
-25 -20 -15

Leu Leu Cys Pro Leu Ser Arg Gly Cys Cys Pro Leu Leu Leu Ser Xaa
-10 -5 1 5

Pro Leu Xaa Gly Val Asn Leu Glu Ser Ile Leu Ser Leu Thr Leu Pro
 10 15 20
 Pro Ser Pro Ser Ser Val Gly Leu Ser Pro Ser Val Thr Xaa Leu Thr
 25 30 35
 Thr Ser Pro Val Ser Leu His Phe Ala Ser Xaa Leu Ala Gly
 40 45 50

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5
seq AALLLGMMVVTG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
 -20 -15 -10
 Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
 -5 1 5 10
 Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
 15 20 25
 Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
 30 35 40
 Xaa Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
 45 50 55
 Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
 60 65 70
 Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
 75 80 85 90
 Trp Leu Val Thr Asp Ile Lys Gly Ala
 95

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq VHLLSLCSGKVYA/RM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
 -20 -15 -10

Leu Cys Ser Gly Lys Val Tyr Ala Arg Met Ala Ser Leu Arg Gly Leu
 -5 1 5

Gly

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 -25 -20 -15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 -10 -5 1

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 5 10 15
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 20 25 30 35
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 40 45 50
 Glu Ser Lys Cys Ala Leu Val Thr Phe
 55 60

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq IVSLLGFVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile
 -25 -20 -15
 Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe
 -10 -5 1
 Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys
 5 10 15 20
 Thr Ser Gln

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/OK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```

Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
      -15                      -10                      -5

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
      1                      5                      10

Gly Asp Leu Gly Ile Val Glu Xaa Thr Cys Ala Thr Asp Leu Gln Thr
      15                      20                      25

Lys Ala Asp Arg Leu Ala Gln Met Xaa Ile Cys Ser Ser Leu Ala Arg
  30                      35                      40                      45

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Xaa
      50                      55                      60

Glu Val Asp Gln Glu
      65

```

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq VHL~~L~~SLCSGKAIC/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
-20 -15 -10

Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr
-5 1 5

Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys
 10 15 20
 Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr
 25 30 35 40
 Xaa Arg Leu Ala Leu Leu Val
 45

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq ALXVLP LLGLHEA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Ala Asp Thr Thr Pro Asn Gly Pro Gln Gly Ala Gly Ala Val Gln
 -50 -45 -40
 Phe Met Met Thr Asn Lys Leu Asp Thr Ala Met Trp Leu Ser Arg Leu
 -35 -30 -25 -20
 Phe Thr Val Tyr Cys Ser Ala Leu Xaa Val Leu Pro Leu Leu Gly Leu
 -15 -10 -5
 His Glu Ala Ala Ser Phe Tyr Gln Arg Ala Leu Leu Ala Asn Ala Leu
 1 5 10
 Thr Ser Ala Leu Arg Leu His Gln Arg Leu Pro His Phe Gln Leu Ser
 15 20 25
 Arg Ala Phe Leu Ala Gln Ala Leu Leu Glu Asp Ser Cys His Tyr Leu
 30 35 40 45
 Leu Tyr Ser Leu Ile Phe Val Asn Ser Tyr Pro Val Thr Met Ser Ile
 50 55 60
 Phe Pro Val Leu Leu Phe
 65

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq XVLVLSVVXXAMA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Arg Phe Arg His Phe Xaa Lys Xaa Ile Gly Xaa Val Leu Val Leu
 -20 -15 -10

Ser Val Val Xaa Xaa Ala Met Ala Ala Phe Ala Val Xaa Pro Gln Gly
 -5 1 5

Pro Ala Leu Xaa Ser Glu Pro Xaa Xaa Xaa Gly Ser Pro Thr Ser Pro
 10 15 20

Lys Pro Gly Val Asn Ala Gln Phe Leu Pro Gly Phe Leu Met Gly Xaa
 25 30 35 40

Leu Pro Ala Pro Val Thr Pro Gln Pro
 45

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LCVEFASVASCDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
 -40 -35 -30 -25
 Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe
 -20 -15 -10
 Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
 -5 1 5
 Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
 10 15 20
 Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu
 25 30 35 40
 Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr
 45 50 55
 Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser
 60 65 70
 Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn
 75 80 85
 Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser
 90 95 100
 Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr
 105 110 115 120
 Leu

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -122..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq RLVVVSVPQSRA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

Met Ala Ser Pro Phe Ser Gly Ala Leu Gln Leu Thr Asp Leu Asp Asp
 -120 -115 -110

```

Phe Ile Gly Pro Ser Gln Glu Cys Ile Lys Pro Val Lys Val Glu Lys
-105                      -100                      -95

Arg Ala Gly Ser Gly Val Ala Lys Ile Arg Ile Glu Asp Asp Gly Ser
-90                      -85                      -80                      -75

Tyr Phe Gln Ile Asn Gln Asp Gly Xaa Thr Arg Arg Leu Glu Lys Ala
                      -70                      -65                      -60

Lys Val Ser Leu Asn Tyr Cys Xaa Ala Cys Ser Gly Cys Ile Thr Ser
                      -55                      -50                      -45

Ala Glu Thr Val Leu Ile Thr Gln Gln Ser His Glu Glu Leu Lys Lys
                      -40                      -35                      -30

Val Leu Asp Ala Asn Lys Met Ala Ala Pro Ser Gln Gln Arg Leu Val
-25                      -20                      -15

Val Val Ser Val Ser Pro Gln Ser Arg Ala Ser Leu Ala Ala Arg Phe
-10                      -5                      1                      5

Gln Leu Xaa Pro Thr Asp Thr Ala Arg Lys Leu Thr Ser Phe Phe Lys
10                      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLVAELLGAGSG/SH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Gly Pro Val Pro Thr Ala Val Ala Gly Ala Gly Ser Arg Leu Val
                      -40                      -35                      -30

Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser
-25                      -20                      -15

Leu Val Ala Glu Leu Leu Leu Gly Ala Gly Ser Gly Ser His Leu Gly
-10                      -5                      1

Arg Ala Trp Ser Gly Leu Gly Ser Ser Ile Ile Glu Ala Ile Val Gly
5                      10                      15                      20

```

Val Leu Leu Thr Ile Arg Pro Ser Arg Leu Glu Pro Pro Tyr His Trp
 25 30 35
 Thr Ser Pro Ala
 40

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq QFILLGTTSVVTA/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
 -20 -15 -10
 Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
 -5 1 5
 Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
 10 15 20 25
 Glu Asp Leu Lys Ser Ile Leu Ser Glu Xaa Pro Gly Lys Cys Val Pro
 30 35 40
 Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
 45 50 55
 Ser Gln Phe Val Glu Asn Cys Lys
 60 65

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq IYIICFXLPPLFS/FN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Gln Val Cys Arg Cys Ile Tyr Ile Ile Cys Phe Xaa Leu Pro Pro
 -15 -10 -5

Leu Phe Ser Phe Asn
 1

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq QRLLLRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Ala Gln Arg Leu Leu Leu Arg Phe Leu Ala Ser Val Ile Ser Arg
 -15 -10 -5 1

Lys Pro Ser Gln Gly Gln Trp Ala Thr Pro His Phe Gln Ser Pro Ala
 5 10 15

Asp Pro Thr Met Gln Ser Trp Trp Pro Asp Cys Asn Thr Gln Pro Ser
 20 25 30

Pro Asp
 35

(2) INFORMATION FOR SEQ ID NO: 474:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -40..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq FLWLITRPQVLP/LL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Met Leu Phe Ile Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala
-40 -35 -30 -25

Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile
 -20 -15 -10

Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Xaa
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 475:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -46..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq SHMLQLLPKALC/LF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Tyr Pro Lys Trp Glu Ala Pro Val Thr Phe Cys Gln Leu Lys Arg
-45 -40 -35

Glu Lys Asp Pro Pro His Pro Ala His Ser Pro Phe Leu Gln Pro Arg
-30 -25 -20 -15

Phe Ser His Met Leu Gln Leu Leu Pro Ser Lys Ala Leu Cys Leu Phe
 -10 -5 1

Phe

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq LAERLGLFEELWA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Ala Leu Tyr Gln Arg Trp Arg Cys Leu Arg Leu Gln Gly Leu Gln
 -40 -35 -30

Ala Cys Arg Leu His Thr Ala Val Val Ser Thr Pro Pro Arg Trp Leu
 -25 -20 -15

Ala Glu Arg Leu Gly Leu Phe Glu Glu Leu Trp Ala Ala Gln Val Lys
 -10 -5 1

Arg Leu Ala Ser Met Ala Gln Lys Glu Pro Gln Thr
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 13.8
seq XGLLLFLLPGSLG/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Gly Val Pro Arg Pro Gln Pro Trp Ala Xaa Gly Leu Leu Leu Phe
   -20                      -15                      -10

Leu Leu Pro Gly Ser Leu Gly Ala Glu Ser His Leu Ser Leu Leu Tyr
   -5                      1                      5

His Leu Thr Ala Val Ser Ser Pro Ala Pro Gly Thr Pro Ala Phe Trp
  10                      15                      20                      25

Val Ser Gly Trp Leu Gly Pro Gln Gln Tyr Pro Ser Xaa
          30                      35

```

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4
seq LVLALXLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

```

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45                      -40                      -35                      -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
   -25                      -20                      -15

Leu Val Leu Ala Leu Xaa Leu Val Ser Ala Ala Leu Ser Ser Val Val
   -10                      -5                      1

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser
  5                      10                      15

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser
  20                      25                      30                      35

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Xaa Xaa Ser Thr Lys Xaa
   40                      45                      50

```


Ser Gly Gly Ala Xaa Val Val Pro His Pro Ser Pro Gly
 55 60

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13
seq LLLVLLLVTXRS/MP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -25 -20 -15

Leu Leu Leu Val Leu Leu Leu Val Thr Arg Xaa Arg Ser Met Pro Ala
 -10 -5 1

Ser Ser Pro Ala Ala Ser Ser Phe Tyr Cys Ala Ser Ser Ala Xaa Ser
 5 10 15

Arg Cys Pro Leu Ala Gly Pro Cys Arg Cys Ser Ser Pro Gly Thr Ala
 20 25 30 35

Phe Leu

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6
seq LLLLVQLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```

Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
      -25                      -20                      -15

Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
      -10                      -5                      1

Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
      5                      10                      15                      20

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
      25                      30                      35

Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
      40                      45                      50

Ala Arg

```

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -20..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20                      -15                      -10                      -5

Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
      1                      5                      10

Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
      15                      20                      25

Gly Asp Gln Leu Ile Trp Thr Arg
      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

```
Met Ser Asn Tyr Thr Asp Ala Glu Ser Ser Phe Ser Lys Gln Glu Ile
-40                               -35                -30                -25

Ile Arg Val Ala Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu
                -20                -15                -10

Val Ala Leu Ser Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly
                -5                1                5

Ala Lys Lys Asp Thr Lys Asp Ser Arg Pro Lys Pro Pro Arg
10                15                20
```

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -53..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6
seq FILLIFIAEVAA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

```

Met Gln Phe Xaa Thr Trp Ala Thr Ser Ser Ser Gln Pro Ala Leu Trp
      -50                -45                -40

Ser Leu Leu Leu Val Ser Trp Ala Ala Met Val Leu Arg Leu Arg Ser
      -35                -30                -25

Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile Phe Ile
      -20                -15                -10

Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Xaa Thr Met Xaa
      -5                  1                  5                  10

Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr
      15                  20                  25

Gly Ser Gln Glu Asp Phe Thr Gln Val Xaa Asn Thr Thr Met Lys Gly
      30                  35                  40

Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Trp
      45                  50                  55

```

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -28..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 10.5
- seq LLLLVHLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

```

Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
      -25                -20                -15

Leu Leu Leu Val His Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
      -10                -5                  1

Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
      5                  10                15                20

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
      25                30                35

Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Xaa Ser Leu Val Leu Ser
      40                45                50

```

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
 55 60 65

Asn Gly Asn Leu Xaa Glu Lys Asp Ile Leu Val Leu Pro Leu Gly
 70 75 80

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.3
seq VSCLTLWSPGCWP/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Thr Thr Phe Leu Pro Val Pro Gln Met Met Ala Gly Phe Ser Phe
 -50 -45 -40

Gly Thr Phe Gly Asn Pro Pro Met Glu Ser Pro Ser Ala Trp Gln Thr
 -35 -30 -25 -20

Ile His Gln Pro Phe Ile Val Ser Cys Leu Thr Leu Trp Ser Pro Gly
 -15 -10 -5

Cys Trp Pro Gln Pro Ile Gln Arg Lys Glu Trp Asp Ser Gly Thr Phe
 - 1 5 10

Glu Asn Leu Arg Val Leu Ser Cys Ala Met Val Glu
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -28..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.5
 seq LVXFSLLATAILG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln Leu
 -25 -20 -15

Val Xaa Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser Trp
 -10 -5 1

Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu Pro
 5 10 15 20

Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys Leu
 25 30 35

Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys
 40 45 50

Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln Glu
 55 60 65

Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe Phe
 70 75 80

Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly
 85 90 95 100

Leu

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.3
 seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

Met Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
-20                -15                -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
-5                1                5                10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Xaa Pro Ile Pro Ser
                15                20                25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
                30                35                40

Ile Phe Leu Lys Phe Asp Gly Glu Arg
                45                50

```

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -109..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1
seq LVLAVLFFHQLVG/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```

Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val Ala Leu
-105                -100                -95

Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu
-90                -85                -80

Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Xaa Lys Ser Tyr Val
-75                -70                -65

Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu
-60                -55                -50

Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr
-45                -40                -35                -30

Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu
-25                -20                -15

Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu
-10                -5                1

```

Lys

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq LLLLCALHSHIYC/IK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Met Pro Asn Leu Ser Phe Gly Gly Leu Asp Thr Asn Gln Met Arg Val
-35 -30 -25

Asn Phe Leu Ser Val Asp Val Cys Lys Leu Leu Leu Leu Cys Ala Leu
-20 -15 -10

His Ser His Ile Tyr Cys Ile Lys Gln Ser Ala Leu Arg
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq XXLLLLNVGQLLA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:


```

Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu
-55          -50          -45          -40

Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu
          -35          -30          -25

Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Xaa Xaa Leu Leu Leu Leu
          -20          -15          -10

Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr
          -5          1          5

Arg Lys Lys Thr Leu Ser Thr
10          15

```

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -71..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6
seq VVXFLLLLAXLIA/TY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```

Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
-70          -65          -60

Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
-55          -50          -45          -40

Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
          -35          -30          -25

Thr Ser Lys Leu Trp His Arg Xaa Xaa Ile Val Val Xaa Phe Leu Leu
          -20          -15          -10

Leu Leu Ala Xaa Leu Ile Ala Thr Tyr Tyr
          -5          1

```

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.6
seq LLRGLLWXQVLCA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Pro Leu Leu Arg Gly Leu Leu Trp Xaa Gln Val Leu Cys Ala Gly
-15 -10 -5 1

Pro Leu His Thr Glu
5

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.4
seq AVVGCLLVPPAEA/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
-20 -15 -10 -5

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Xaa Cys Lys Cys Ile
1 5 10

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
15 20 25

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
30 35 40

Pro
45

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
 -20 -15 -10
Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
 -5 1 5
Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala
 10 15 20
Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala
 25 30 35 40
Val Gly Glu Lys Arg
 45

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -108..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.9
 seq LLGLLSAEQLAEA/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```

Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
      -105                -100                -95

Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
      -90                -85                -80

Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
      -75                -70                -65

Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
      -60                -55                -50                -45

Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
      -40                -35                -30

Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Xaa Xaa Val Gln Leu
      -25                -20                -15

Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
      -10                -5                1

Leu Phe Asn Lys Ile Asp Asn
  5                10
  
```

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -41..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.7
 seq LLCLGQLHHPGLG/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

```

Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser Pro Arg Ser Leu
      -40                -35                -30

Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg Leu Leu Cys Leu
  
```

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq PTLAIALAANAWA/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

```

Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp
      -25                -20                -15

Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu
      -10                -5                1

Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu
      5                10                15

Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg Asp Leu
      20                25                30

```

(2) INFORMATION FOR SEQ ID NO: 499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -32..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.6
seq WILVLALPLTVWP/WL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```

Met Gln Gln Ile Phe Ile Gln Gln Cys Arg Glu Leu Asn Phe Trp Ser
      -30                -25                -20

Arg Glu Pro Trp Ile Leu Val Leu Ala Leu Pro Leu Thr Val Trp Pro
      -15                -10                -5

Trp Leu Ser Pro Glu Ala Gln Pro Pro Leu
      1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq AVLLALLMAGLAL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
-15 -10 -5 1
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Trp Xaa Ala Gln Val Xaa Asn
5 10 15
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
20 25 30
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
35 40 45
Gly Cys Ser Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly
50 55 60 65
Lys Lys Asn Ile Thr Cys Cys Asp
70

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq QACLLGLFALILS/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu Ser
 -15 -10 -5
 Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu Pro
 1 5 10 15
 Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser
 20 25 30
 Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu
 35 40 45
 Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr Leu
 50 55 60
 Thr Arg
 65

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq LGSGLGLSPGTSS/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Pro Gly Gln Val Ser Leu Leu Gly Pro Asp Ala Val Ser Val
 -25 -20 -15
 Leu Gly Ser Gly Leu Gly Leu Ser Pro Gly Thr Ser Ser Gly Arg Asn
 -10 -5 1
 Pro Asp Pro Gly Ser Gly Pro Gly Thr Leu Pro Xaa Xaa Ser Xaa Gln
 5 10 15
 Asn Pro Ser Pro Ala Pro Asp Pro Pro Pro Ala Leu Leu Leu Trp Asn
 20 25 30 35
 Leu Leu Thr Gln Arg Leu Gly Thr Thr Leu Val Pro Thr Leu Cys Pro
 40 45 50
 Ala Gln Thr Leu Ile Leu Cys Pro Ala Gln Thr Leu Ile Leu Cys Pro
 55 60 65

Xaa Leu Ile Pro Thr Leu Cys Pro Ala Leu Xaa Pro Val Leu Pro Xaa
70 75 80
Val Ala Leu Ser Ala Gln Pro Ser Leu Pro Ala Arg Val Gln Ser
85 90 95

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8
seq FTSASLLLPSTG/MP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Ile Asn Pro Ser Val Pro Ser Lys Ser Asn Ser His Pro Phe Leu
-30 -25 -20
Ser Thr Val Met Phe Thr Ser Ala Ser Leu Leu Leu Pro Met Ser Thr
-15 -10 -5
Gly Met Pro Thr Gln Asn Cys Phe Thr Pro Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7

seq IACLAWWIGGGSG/XN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

```

Met Ser Glu Lys Glu Xaa Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro
      -65                      -60                      -55

Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu
      -50                      -45                      -40

His Gln Val Leu Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys
      -35                      -30                      -25

Ala Thr Leu Gly Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly
      -20                      -15                      -10                      -5

Gly Gly Ser Gly Xaa Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Leu
              1                      5                      10

Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala
              15                      20                      25

Phe Arg Ala Asp Ser Ser Phe Asn Phe Met Ala Leu
      30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ILRLYFFLQLAHS/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

```

Met Asn Pro Thr Lys Leu Ile Leu Lys Thr Ile Leu Arg Leu Tyr Phe
      -20                      -15                      -10

Phe Leu Gln Leu Ala His Ser Gly Tyr Thr Lys Leu Gln Lys Lys Tyr
      -5                      1                      5

Met Lys Ser Arg Tyr Glu Gln Val Asp Leu Val Gly Lys Met Xaa Gln
      10                      15                      20                      25

Lys Ala Ala Thr Thr Val Xaa His Leu Ala Ile Gln Cys His Trp

```

30

35

40

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq SXXCFVSVPPASA/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

```

Met Ala Ser Ser Ser Pro Asp Ser Pro Cys Ser Xaa Xaa Cys Phe Val
      -20                      -15                      -10

Ser Val Pro Pro Ala Ser Ala Ile Pro Xaa Val Xaa Xaa Ala Xaa Asn
      -5                      1                      5

Ser Asp Xaa Pro Arg Asp Glu Val Gln Glu Val Val Phe Val Pro Ala
    10                      15                      20                      25

Gly Thr His Thr Pro Gly Ser Arg Leu Gln Cys Thr Tyr Ile Glu Val
      30                      35                      40

Glu Gln Val Ser Lys Thr His Ala Val Ile Leu Ser Arg Pro Ser Trp
      45                      50                      55

Leu Trp Gly Ala Glu Met Gly Xaa Thr Ser Met Val Ser Ala Leu Ala
      60                      65                      70

Thr Arg Leu Cys Gly Arg Arg Ser Gln Leu Gly Arg Ala Xaa Ala Leu
      75                      80                      85

Leu Gly Met Asp Leu Leu Arg Cys Arg Pro Cys
      90                      95                      100

```

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -39...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq XLIAXLEPPGAMA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

```

Met Xaa Pro Val Leu Ala Ala Leu Ala His Val Leu Cys Pro Tyr Met
      -35                -30                -25
Ala Pro Gly Leu Cys Arg Glu Pro Ile Arg Xaa Leu Ile Ala Xaa Leu
      -20                -15                -10
Glu Pro Pro Gly Ala Met Ala Val Arg Arg Leu Pro Ser Ala
      -5                  1                  5
  
```

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -45...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq PMLGLAAFRWIWS/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

```

Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg Pro Asn Ser
-45                -40                -35                -30
Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala Leu Leu Val
      -25                -20                -15
Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser Arg Glu Ser
      -10                -5                  1
Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg Arg Thr Ala
  5                  10                  15
  
```

Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met Ile Ser Xaa
20 25 30 35
Asn Arg Arg Ala Val
40

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq AALCSLFFFLSLQ/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Leu Leu Leu Phe Leu Ala Ala Leu Cys Ser Leu Phe Phe Phe Leu
-15 -10 -5
Ser Leu Gln Glu Ile Ala Pro Gln Asp Pro Lys Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq IIVCLFAFLVAHC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

```

Met Leu Phe Leu Gly Lys Val Leu Ile Val Cys Ser Thr Gly Leu Ala
  -45                               -40                               -35

Gly Ile Met Leu Leu Asn Tyr Gln Gln Asp Tyr Thr Val Trp Val Leu
  -30                               -25                               -20

Pro Leu Ile Ile Val Cys Leu Phe Ala Phe Leu Val Ala His Cys Phe
-15                               -10                               -5                               1

Leu Ser Ile Tyr Glu Met Val Val Asp Ala Arg
      5                               10

```

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(3) LOCATION: -38..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq LLLLVHSFWFTVC/TP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Gln Gly Ile Pro Ile Leu Thr Pro Val Thr Thr Gln Ser Ile Ala
-35 -30 -25

Ile Ser Ile Val Leu Thr Val Gln Gly Leu Leu Leu Leu Val His Ser
-20 -15 -10

Phe Trp Phe Thr Val Cys Thr Pro Val Val Phe
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
(B) TYPE: AMINO ACID
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq LFCVLLSLRPHTS/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

```

Met Gln Asn Phe Cys His His Leu Ala Ile Cys Thr Val Ile Leu Phe
  -25                      -20                      -15

Cys Val Leu Leu Ser Leu Arg Pro His Thr Ser Gly Thr Leu Trp Ala
  -10                      -5                      1                      5

Ser Ser Ala His Gly Leu His Leu Ala Pro Ala Glu Pro Gln Leu Ser
          10                      15                      20

Cys Trp Met Cys Cys Ala
          25

```

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

```

Met Pro Ser Phe Ser Lys Asp Leu Leu Thr Val Pro Lys Leu Gly Thr
          -60                      -55                      -50

Gly His Xaa Xaa Gly Xaa Gly Ser Tyr Asp Xaa Ala Leu Xaa Leu Leu
          -45                      -40                      -35

Leu Lys Cys Leu Trp Ser Asn Val Val Pro Glu Cys Thr Met Ala Ser
          -30                      -25                      -20

Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr Ser Ile Ala
          -15                      -10                      -5

Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu Gly Asp Leu

```

```

1           5           10           15
Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr Lys Ala Asp
                20                25                30
Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Xaa Xaa Lys Phe Pro
                35                40                45
Lys Leu Xaa Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu Glu Val Asp
                50                55                60
Gln Glu Leu Ile Glu Asp Xaa
    65                70

```

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq LEMLXAFASHIXA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Xaa Ala Phe Ala
-20 -15 -10
-
Ser His Ile Xaa Ala Arg Asp Ala Ala Gly Ser Gly
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -139..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq FGLLHQLSQCVTS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

Met Glu Val Gly Leu Pro Ala Ile Thr Leu Phe Leu Thr Ser Ala Ser
 -135 -130 -125
Ser Pro Val Val Ala Thr Thr Met Asp Gln Glu Pro Val Gly Gly Val
 -120 -115 -110
Glu Arg Gly Glu Ala Val Ala Ala Ser Gly Xaa Ala Ala Ala Ala Ala
 -105 -100 -95
Phe Gly Glu Ser Ala Gly Gln Met Ser Asn Glu Arg Gly Phe Glu Asn
 -90 -85 -80
Val Glu Leu Gly Val Ile Gly Lys Lys Lys Lys Val Pro Arg Arg Val
 -75 -70 -65 -60
Ile His Phe Val Ser Gly Glu Thr Met Glu Glu Tyr Ser Thr Asp Glu
 -55 -50 -45
Asp Xaa Val Asp Gly Leu Glu Lys Xaa Met Phe Cys Leu Leu Leu Ile
 -40 -35 -30
Arg Gln Asn Leu Pro Gly Val Pro Thr Tyr Gly Phe Thr Cys Phe Gly
 -25 -20 -15
Leu Leu His Gln Leu Ser Gln Cys Val Thr Ser Leu Glu
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -43..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq SAATLASLGGTSS/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Met Lys Glu Leu Glu Arg Gln Gln Lys Glu Val Glu Glu Arg Pro Glu
 -40 -35 -30

Lys Asp Phe Thr Glu Lys Gly Ser Arg Asn Met Pro Gly Leu Ser Ala
 -25 -20 -15

Ala Thr Leu Ala Ser Leu Gly Gly Thr Ser Ser Arg Arg Gly Ser Gly
 -10 -5 1 5

Asp Thr Ser Ile Ser Ile Asp Pro Glu
 10

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq VLVILCIVTVCVT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Ser Met Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile Val
 -20 -15 -10

Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu
 -5 1 5 10

Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala
 15 20 25

Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys
 30 35 40

Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val
 45 50 55

Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile
 60 65 70

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -70..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLFPLTLVRSEWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Met Glu Leu Xaa Leu Lys Xaa Xaa Thr Lys Xaa Glu Xaa Glu Ser
-70 -65 -60 -55
Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala Cys His
-50 -45 -40
Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln
-35 -30 -25
Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu
-20 -15 -10
Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Xaa
-5 1 5 10
Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Xaa Gly Xaa Ile Val
15 20 25
Ile Xaa Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln
30 35 40
Glu

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6
seq GLILLFASHLINQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Val Ser Asn Ala Ser Glu Thr Ser Cys Leu Gly Leu Ile Leu Leu
-20 -15 -10

Phe Ala Ser His Leu Ile Asn Gln Phe Ser Ser
-5 1

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq LIVFISVCTALLA/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
-70 -65 -60

Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
--55 -50 -45

Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
-40 -35 -30

Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
-25 -20 -15 -10

Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
-5 1 5

Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
10 15 20

Gln Ser Lys Lys Tyr Leu Met Val Glu Trp Trp Gln Xaa Phe Leu Phe
25 30 35

Tyr Pro Ser Phe Leu Xaa Pro Lys Xaa Val Ser Ser
40 45 50

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LGAAALALLANT/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Gly Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu
-20 -15 -10

Ala Leu Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys
-5 1 5

Ala Ala Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys
10 15 20 25

Glu Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala
30 35 40

Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu
45 50 55

Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val
60 65 70

Pro Leu Tyr Ala Val Val Lys Glu Gln Arg
75 80

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LPLLLVANAGTAA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Asp Val Ala Phe Leu Glu Xaa Leu Ile Lys Asp Asp Ile Glu Arg
-30 -25 -20

Gly Arg Leu Pro Leu Leu Leu Val Ala Asn Ala Gly Thr Ala Ala Val
-15 -10 -5 1

Gly His Thr Asp Lys Ile Gly Arg Leu Lys Glu Leu Cys Glu Gln Tyr
5 10 15

Gly Ile Trp Leu His Val Glu Gly Val Asn
20 25

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LFNLLWLALACSP/VW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5

Val Trp
1

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -33..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.8
seq FICLQWALPHSEA/GD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

```

Met Asn Ala Gln Pro Gly Leu Xaa Leu Asp Cys Ile Thr Arg Phe Leu
      -30              -25              -20
Thr Xaa Gly Gln Phe Ile Cys Leu Gln Trp Ala Leu Pro His Ser Glu
      -15              -10              -5
Ala Gly Asp Phe Glu Ala Lys
  1              5

```

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -69..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq LCRLCLVRLFCC/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

```

Met Gly Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala
      -65              -60              -55
Pro Ala Trp Gly Ala Gly Pro Pro Val His Pro Ala Pro Pro Pro Val
      -50              -45              -40
Glu Lys Thr Leu Ser Trp Gly Cys Gly Phe Gly Leu His Ser Gly Phe
      -35              -30              -25
Gly Gly Ser Gly Gly Gly Val Gly Leu Cys Arg Leu Leu Cys Leu Val

```

-10

-5

(i) SEQUENCE CHARACTERISTICS:

- (vi) ORIGINAL SOURCE:

- (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

-25

-20

-15

-10

-5

1

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Ile Ala Ile Tyr Gly Lys Asn Phe Cys Val Ser Ala Lys Asn Ala
 -45 -40 -35

Phe Met Leu Leu Met Arg Asn Ile Val Arg Val Val Val Leu Asp Lys
 -30 -25 -20

Val Thr Asp Leu Leu Leu Phe Phe Gly Lys Leu Leu Val Val Gly Gly
 -15 -10 -5

Val Gly Val Leu Ser Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly Leu
 1 5 10 15

Gly Lys Asp Phe Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro Xaa
 20 25 30

Met Thr Ser Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe Ser
 35 40 45

Val Phe Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu Asp
 50 55 60

Leu Glu Arg Thr Thr Ala Pro Trp Thr Ala Leu Leu His Val Gln Glu
 65 70 75 80

Leu Leu

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -91..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq SVLELIVASVCQS/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Glu Arg Asn Cys Lys Gly Ser Phe Gly Val Ile Lys Glu Gly Asp
 -90 -85 -80

Thr Asp Thr Xaa Glu Thr Lys Ala Arg Arg Thr Val Trp Glu Pro Arg
 -75 -70 -65 -60

Gly Arg Tyr Ser Phe Arg Xaa Thr Pro Arg Pro Ala Tyr Pro Val Glu
 -55 -50 -45

Gln Cys Gly Phe Ala Arg Arg Ala Leu Glu Leu Leu Glu Ile Arg Lys
 -40 -35 -30

His Ser Pro Glu Val Cys Glu Pro Pro Asn Ile Pro Val Thr Ser Val
 -25 -20 -15

Leu Glu Leu Ile Val Ala Ser Val Cys Gln Ser His Ile Arg Thr Thr
 -10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -66...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LYMLAEALPVSHG/AH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Phe Val Glu Tyr Arg Lys Gln Leu Lys Leu Leu Leu Asp Arg Leu
 -65 -60 -55

Ala Gln Val Ser Pro Glu Leu Leu Leu Ala Ser Val Arg Arg Val Phe
 -50 -45 -40 -35

Ser Ser Thr Leu Gln Asn Trp Gln Thr Thr Arg Phe Met Glu Val Glu
 -30 -25 -20

Val Ala Ile Arg Leu Leu Tyr Met Leu Ala Glu Ala Leu Pro Val Ser
 -15 -10 -5

His Gly Ala His Phe Ser Gly Asp Val Ser Lys Ala Ser Ala Leu Gln
 1 5 10

Asp Met Met Arg Thr Leu Val Thr Ser Gly Val Ser Gly
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq IIFLIQWHGVSFQ/EF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Leu Leu Gly Thr Ser Asn Ile Ile Ile Phe Leu Ile Gln Trp His
-20 -15 -10
Gly Ser Val Phe Gln Glu Phe
-5 1

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq AFVXACVLSLIST/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Xaa Asn Arg Phe Ala Thr Ala Phe Val Xaa Ala Cys Val Leu Ser
-20 -15 -10 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
1 5 10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
15 20 25
Ser Ile Trp Asp Glu Leu
30

(2) INFORMATION FOR SEQ.ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq MSLTSGFLRVSQG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

```

Met Ser Leu Thr Ser Gly Phe Leu Arg Val Ser Gln Gly Ser Pro Asn
      -10                      -5                      1
Leu Ser Gln
      5

```

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq AIRTLFSVTGILA/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

```

Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile
      -60                      -55                      -50
Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His
      -45                      -40                      -35

```

Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val
 -30 -25 -20

Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu
 -15 -10 -5 1

Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His
 5 10 15

Trp Ile Lys Leu Met Asn
 20

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq AGLLFGLAGLGA/YQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
 -50 -45 -40

Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
 -35 -30 -25

Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
 -20 -15 -10 -5

Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
 1 5 10

Phe Leu Ala Thr Ser Gly Thr Leu Ala
 15 20

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -35..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq CCALLTSLXCIWG/PA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

```

Met Glu Xaa Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
-35                -30                -25                -20

Thr Xaa Xaa Xaa Xaa Tyr Cys Cys Ala Leu Leu Thr Ser Leu Xaa Cys
          -15                -10                -5

Ile Trp Gly Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys
          1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq ITGVILLAVGIWG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

```

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
          -40                -35                -30

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
          -25                -20                -15

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
          -10                -5                1                5

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
          10                15                20

```

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Leu
25 30 35

(2) INFORMATION FOR SEO ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -67..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
seq LSVSLLPAGAWs/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

```

Met Phe Ser Arg Glu Leu Ala Pro Thr Arg Ile Gly Gly Ala Ser Ser
    -65                                -60                                -55

Gly Ser Arg Ser Gly Gly Thr Leu Ile Ser Thr Ala Pro Leu Thr Thr
    -50                                -45                                -40

Arg Val Leu Asn Pro Thr Ala Gln Cys Phe Cys Leu Asp Cys Thr Leu
-35                                -30                                -25                                -20

Arg Arg Met Gln Thr His Leu Ser Val Ser Leu Leu Pro Cys Ala Gly
                                -15                                -10                                -5

Ala Trp Ser Leu Leu Xaa Ser Lys Lys Val Ile Leu Pro Ser Cys Ser
          1                                5                                10

Ser Ile Leu Xaa Thr Val Val Val Ile
    15                                20

```

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq LLMLGVTLPSYW/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

```

Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
      -25                      -20                      -15

Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
      -10                      -5                      1

Thr Val His Gly Asn Val Ile Xaa Thr Asn Xaa Ile Phe Glu Asn Leu
    5                      10                      15

Trp Phe Ser Ser Ala Gly
  20                      25

```

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq XFLXLXXLSXXWP/XD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Glu Lys Ile Pro Val Ser Xaa Phe Leu Xaa Leu Xaa Xaa Leu Ser
-20                      -15                      -10                      -5

Xaa Xaa Trp Pro Xaa Asp Thr Thr Val Lys Pro Gly Ala Xaa Lys Asp
      1                      5                      10

Thr Lys Asp Ser Arg Xaa Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
    15                      20                      25

Gly Asp Gln Leu Ile Trp Thr Arg
    30                      35

```


(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -67..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq LILERPLVPSAEA/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met His Ser Ala Glu Glu Pro Leu Xaa Leu Ala Ala Leu Arg Gly Ala
-65 -60 -55

Arg Gly His Leu Pro Cys Gly Ser Arg His His Val Gly Ser Leu Ala
-50 -45 -40

Pro Ala Ser Val Pro Ala Pro Gly Ala Cys Leu Trp Val Cys Glu Trp
-35 -30 -25 -20

Glu Thr Leu Leu Pro Gly Leu Ile Leu Glu Arg Pro Leu Val Pro Ser
-15 -10 -5

Ala Glu Ala Ser Gly Ala Gly Lys Leu Ser Arg Lys Glu Ala Leu Leu
1 5 10

Ser Asn Tyr Ala Leu
15

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.9
seq GLWLALVDGLVRX/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

```

Met Ala Gly Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu
      -40              -35              -30

Ser Gln Ile Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu
      -25              -20              -15

Trp Leu Ala Leu Val Asp Gly Leu Val Arg Xaa Ala Pro Arg Trp Ile
      -10              -5              1              5

Xaa Gly

```

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -78..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq VGAVFGLTTCISA/HV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

```

Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
      -75              -70              -65

Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
      -60              -55              -50

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
      -45              -40              -35

Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
      -30              -25              -20              -15

Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
      -10              -5              1

Arg Glu Lys Pro Asp Asp Pro Leu Asn Arg
      5              10

```

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq WLQVLPVILLLLG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
-15 -10 -5

Leu Gly Val Pro Pro Ser
1

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LLILDMNVLYTDA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Glu Ile Tyr Phe Ile Phe Cys Ile Ile Val Pro Ile Ala Ala Ala
-35 -30 -25

Thr Val Tyr Lys Ser Trp Cys Leu Leu Leu Ile Leu Asp Met Asn Val
-20 -15 -10

Leu Tyr Thr Asp Ala Ser Pro Leu Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VLLAIGMFFTAWF/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe Pro His Leu
-30 -25 -20

Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala Trp Phe Phe
-15 -10 -5 1

Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile Tyr Lys Glu
5 10 15

Leu Gln

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LMLSSSLPLLIWL/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

```

Met Arg Leu Ala Ala Glu Ala His Pro Gly Arg Thr His Thr Leu Phe
-35          -30          -25          -20

Arg Arg Leu Lys Pro Phe Leu Met Leu Ser Ser Ser Leu Pro Leu Leu
          -15          -10          -5

Ile Trp Leu Lys Asp Arg
          1

```

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq IILFSAIVGFIYG/YV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

```

Met Leu Glu His Leu Xaa Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly
          -35          -30          -25

Gln Lys Leu Ala Xaa Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala
          -20          -15          -10

Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr
          -5          1          5

Val Tyr Ile Val Met Ala Gly
10          15

```

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq SKVLFCFSNVLG/FD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

Met Glu Tyr Ser Lys Val Leu Phe Cys Ser Phe Ser Asn Val Leu Gly
-15 -10 -5

Phe Asp Tyr
1

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
-25 -20 -15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
-10 -5 1 5

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
10 15 20

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Ser Gly
25 30

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LGLALGRLEGGSA/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

```
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
   -50                      -45                      -40

Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
   -35                      -30                      -25

Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
   -20                      -15                      -10                      -5

Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
           1                      5                      10

Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro
   15                      20                      25
```

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LIALTCLDGTTVS/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

```
Met Asn Ala Leu Met Val Leu Phe Asn Val Thr Val Val Leu Ile Ala
```

-25 -20 -15
 Leu Thr Cys Leu Asp Gly Thr Thr Val Ser Ala Glu Met Ala Thr Met
 -10 -5 1 5
 Thr Met Gly Cys Phe His Gln Val Glu Asn Arg Val Lys Ile Leu Met
 10 15 20
 Ser Val Gly Pro Gly Gly Thr Ala Val Pro Met Ile Pro Phe Ala Ser
 25 30 35
 Ile Trp Met Ala Asp Met Ile Xaa Asp
 40 45

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq VLVYLVTAERVWS/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 -45 -40 -35 -30
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 -25 -20 -15
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 -10 -5 1
 Lys

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq SLFIYIFXTCSNT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Xaa Thr Cys Ser Asn Thr
-15 -10 -5

Ser Pro Ser Tyr Gln Xaa Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
1 5 10 15

Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
20 25 30

Cys Phe Xaa Leu Gln
35

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LNSLSALAEAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
-15 -10 -5

Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq TLRTWLCCAGSWA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Thr Ala Gly Thr Leu Arg Thr Trp Leu Cys Cys Ala Gly Ser Trp
-15 -10 -5
Ala Val Glu Leu Pro Ala Glu Pro Leu Val Val Phe Cys Xaa Ser Thr
1 5 10 15
Ser Arg Lys Arg Ala Lys Gly Leu Ile Gln Ser Val
20 25

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq RLLVILCVSVKAG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

Met Leu Gly Arg Pro Cys Phe His Ser Pro Gln Arg Leu Leu Val Ile
-20 -15 -10
Leu Cys Val Ser Val Lys Ala Gly Ser Thr
-5 1

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LQFVLPVATQIIQQ/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

Met Asp Glu Ala Arg Asp Asn Ala Cys Asn Asp Met Gly Lys Met Leu
 -25 -20 -15

Gln Phe Val Leu Pro Val Ala Thr Gln Ile Gln Gln Glu Val Ile Lys
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LCALGSAPSSMWA/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Met Ser Pro Ile Ser Ile Arg Glu Leu Cys Ala Leu Gly Ser Ala Pro
 -20 -15 -10

Ser Ser Met Trp Ala Gly Glu
 -5 1

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq MTDLLSASPWALT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Met Thr Asp Leu Leu Ser Ala Ser Pro Trp Ala Leu Thr Ile Val Ser
-10 -5 1
Ser Glu Leu His Leu Ala Pro Ser Met Thr Thr Val Asp Gln Leu Glu
5 10 15
Ser Gln Val Asp Asn Val Ile Leu Gln Thr Gly Glu Ser Ala Ser Glu
20 25 30 35
Cys Phe Cys Leu Gln Cys Pro Ser Leu Gly Asn Ile Glu Gly Gly Val
40 45 50
Ala Thr Gly His Xaa
55

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2

seq LTCGPALVPRLWA/TC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

Met Ser Trp Ser Gly Leu Leu His Gly Leu Asn Thr Ser Leu Thr Cys
 -25 -20 -15

Gly Pro Ala Leu Val Pro Arg Leu Trp Ala Thr Cys Ser Met Ala Thr
 -10 -5 1 5

Leu Asn Gln Met His Arg Leu Gly Pro Pro Lys Arg Pro Pro Arg Lys
 10 15 20

Leu Gly Pro Thr Glu Gly Arg Pro Gln Leu Lys Gly Val Val Leu Cys
 25 30 35

Thr Phe Thr Arg Asn Arg
 40

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq LEAFSQAISAIQA/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

Met Ala Asp Val Ile Asn Val Ser Val Asn Leu Glu Ala Phe Ser Gln
 -20 -15 -10

Ala Ile Ser Ala Ile Gln Ala Leu Arg Ser Ser Val Ser Arg Val Phe
 -5 1 5

Asp Cys Leu Lys Asp Gly Met Arg Asn Lys Glu Thr Leu Glu Gly Arg
 10 15 20 25

Glu Lys Ala Phe Ile Ala His Phe Gln Asp Asn Leu His Ser Val Asn
 30 35 40

Arg Asp Pro

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His
-30 -25 -20

Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn
-15 -10 -5

Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr
1 5 10 15

His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser
20 25 30

Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq ACLAWTAVRPSAC/CH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

Met Thr Ser Ala Cys Leu Ala Trp Thr Ala Val Arg Pro Ser Ala Cys
 -15 -10 -5

Cys His Pro Gln Ser Ala Asn Trp
 1 5

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq VFGMSSSSGASNS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Asn Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu
 -55 -50 -45 -40

Gln Gly Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Xaa Gln Thr
 -35 -30 -25

Ala Pro Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser
 -20 -15 -10

Ser Ser Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly
 -5 1 5

Ser Lys Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Gly
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FFLFLSFVLMYDG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp Gly
-15 -10 -5

Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr Met
1 5 10 15

Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq SIKVLLQSALS LG/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

Met Met Glu Glu Arg Ala Asn Leu Met His Met Met Lys Leu Ser Ile
-25 -20 -15

Lys Val Leu Leu Gln Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala
-10 -5 1 5

Asp His Ala Pro Leu Gln Gln Phe Phe Val Val Met Glu His Cys Ser
10 15 20

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq XIVSAALLAFVQT/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

```

Met Glu Leu Glu Xaa Ile Val Ser Ala Ala Leu Leu Ala Phe Val Gln
  -15                      -10                      -5

Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe
   1                      5                      10                      15

Ser Tyr Val Xaa Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser
                20                      25                      30

Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Xaa
   35                      40                      45

Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Xaa Met Met
   50                      55                      60

```

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq SLIPLFXFIGTGA/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

```

Met Leu Arg Gln Ile Ile Gly Gln Ala Lys Lys His Pro Ser Leu Ile
  -25                      -20                      -15

```

Pro Leu Phe Xaa Phe Ile Gly Thr Gly Ala Thr Gly Ala Thr Leu Tyr
 -10 -5 1 5
 Leu Leu Arg Leu Ala Leu Phe Asn Pro Xaa Val Cys Trp Asp Arg Xaa
 10 15 20
 Asn Pro Glu Pro Trp Asn Xaa Leu Gly Pro Glu
 25 30

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -98..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq WTSLTCSLVVVDG/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met Val Lys Glu Thr Gln Tyr Tyr Asp Ile Leu Gly Val Lys Pro Ser
 -95 -90 -85
 Ala Ser Pro Glu Arg Ser Arg Arg Pro Ile Gly Ser Trp Arg Ser Ser
 -80 -75 -70
 Thr Thr Arg Thr Arg Thr Arg Met Arg Ala Arg Ser Leu Asn Ser Tyr
 -65 -60 -55
 Pro Arg His Met Lys Cys Phe Gln Ile Gln Arg Lys Gly Met Phe Met
 -50 -45 -40 -35
 Thr Lys Ala Glu Ser Arg Gln Xaa Lys Lys Glu Ala Gln Ala Ala Pro
 -30 -25 -20
 Ala Ser Leu His Pro Trp Thr Ser Leu Thr Cys Ser Leu Val Val Val
 -15 -10 -5
 Asp Gly Cys Gly
 1

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RALSTXLFGSIRG/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn Pro Leu Leu Tyr Leu
-35 -30 -25

Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Xaa Leu Phe Gly
-20 -15 -10 -5

Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala Val
1 5 10

Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala Leu
15 20 25

Gly Phe Lys Asn Lys Thr Val Leu Lys Lys Arg Cys Lys Asp Cys Tyr
30 35 40

Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro
45 50 55 60

Arg His Lys Gln Arg His Met Xaa Thr Leu Ser Leu Gln Ser His Ala
65 70 75

Gln -

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq RIHLCQRSPGSQG/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

Met Ala Ala Ala Ala Ala Ser Arg Gly Xaa Gly Ala Lys Leu Gly Leu
 -30 -25 -20
 Arg Xaa Ile Arg Ile His Leu Cys Gln Arg Ser Pro Gly Ser Gln Gly
 -15 -10 -5
 Val Arg Asp Phe Ile
 1 5

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE: PROTEIN
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
 (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -44..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq IALTLPMSLSRA/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

Met Phe Pro Ser Cys Tyr Leu Cys Tyr Ser Leu Cys Gly Ser Ile Leu
 -40 -35 -30
 Leu Ser Ile Phe Ser Ala Tyr Asn Arg Leu Ser Leu Met Leu Arg Ile
 -25 -20 -15
 Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys
 -10 -5 1
 Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys
 5 10 15 20
 Gly

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids

- (B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -60..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq QLXFLYFVCCIFQ/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Met Ser Thr Gln Xaa Gly Leu Ser Met His Ala His Pro Gln Ala Tyr
-60 -55 -50 -45
Thr Pro Phe Ile Tyr Leu His Ala Arg Lys Arg Arg Gly Glu Ile Gly
-40 -35 -30
Asp Ala Asp Ser Arg Phe Asn Asp Arg Tyr Ala His Lys Ser Ala Gln
-25 -20 -15
Leu Xaa Phe Leu Tyr Phe Val Cys Cys Ile Phe Gln Asp Val Tyr Tyr
-10 -5 1
Xaa
5

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq SSCSCSLISFTRG/DK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

Met Lys His Phe Gln Asp Leu Pro Ser Ser Cys Ser Cys Ser Leu Ile
-20 -15 -10

Ser Phe Thr Arg Gly Asp Lys Tyr Phe Ala Tyr Asn Glu Glu Ile Phe
 -5 1 5 10
 Leu Val Tyr Asn Ala Asp Gln
 15

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -62..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq SILGIISVPLSIG/YC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg
 -60 -55 -50
 Xaa Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys
 -45 -40 -35
 Val Leu Pro His Met Ile Glu Arg Lys Xaa Xaa Lys Ile Val Thr Val
 -30 -25 -20 -15
 Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys
 -10 -5 1
 Ala Ser Xaa His Ala Leu Xaa Gly Phe Phe Asn Xaa Leu Arg Thr Xaa
 5 10 15
 Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser
 20 25

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -98..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LALRTSWISSVCS/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

```

Met Gly Gly Ser Gly Ser Arg Leu Ser Lys Glu Leu Leu Ala Glu Tyr
      -95                      -90                      -85

Gln Asp Leu Thr Phe Leu Thr Lys Gln Glu Ile Leu Leu Ala His Arg
      -80                      -75                      -70

Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln Arg Xaa Xaa Ser Arg His
      -65                      -60                      -55

Phe Gly His Lys Cys Pro Ser Ser Arg Phe Ser Ala Phe Gln Ser Ser
-50                      -45                      -40                      -35

Arg Pro Thr Pro Ser Arg Ser Glu Ser Ala Gly Ser Ser Pro His Pro
      -30                      -25                      -20

Gln Pro Lys Thr Ala Leu Ala Leu Arg Thr Ser Trp Ile Ser Ser Val
      -15                      -10                      -5

Cys Ser Val Thr Gln Pro Arg Gln Thr Ser Ser Pro Ile Met Pro Ser
      1                      5                      10

Ala Ser Leu Thr Leu Met Met Thr
15                      20

```

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq PLSDSWALLPASA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
-25 -20 -15

Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
-10 -5 1

Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
5 10 15 20

Lys Leu Leu

(2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -114..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq ATFVTDALIQXYA/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

Met	Ala	Asp	His	Val	Gln	Ser	Leu	Ala	Gln	Leu	Glu	Asn	Leu	Cys	Lys
				-110					-105					-100	
Gln	Leu	Tyr	Glu	Thr	Thr	Asp	Thr	Xaa	Xaa	Arg	Ser	Ser	Xaa	Ala	Glu
			-95					-90					-85		
Lys	Ala	Leu	Val	Glu	Phe	Thr	Asn	Ser	Pro	Asp	Cys	Leu	Ser	Lys	Cys
		-80					-75					-70			
Gln	Leu	Leu	Leu	Glu	Arg	Gly	Ser	Ser	Ser	Tyr	Ser	Gln	Leu	Leu	Ala
	-65					-60					-55				
Ala	Thr	Cys	Leu	Thr	Lys	Leu	Val	Ser	Arg	Thr	Asn	Asn	Pro	Leu	Pro
-50					-45					-40					-35
Leu	Glu	Gln	Arg	Ile	Asp	Ile	Arg	Asn	Tyr	Val	Leu	Asn	Xaa	Leu	Ala
				-30					-25					-20	
Thr	Arg	Pro	Lys	Leu	Ala	Thr	Phe	Val	Thr	Gln	Ala	Leu	Ile	Gln	Xaa
			-15					-10					-5		
Tyr	Ala	Arg	Ile	Thr	Lys	Leu	Gly	Trp	Phe	Asp					
		1					5								

(2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -55..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq TCSVCCYLEFWLIA/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

```

Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe
-55                      -50                      -45                      -40

Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro
                      -35                      -30                      -25

Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys
                      -20                      -15                      -10

Tyr Leu Phe Trp Leu Ile Ala Ile Pro Ala Trp
      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -58..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
 seq GGILMGSFQGTIA/GO
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

```

Met Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His
-55 -50 -45

Ser Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu
-40 -35 -30

Ile Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile
-25 -20 -15

Leu Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala
-10 -5 1 5

Thr Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly
10 15 20

Ala Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ser
25 30 35

His Pro Ala Leu Ala Ala Thr Ala Phe Ser Leu Xaa Cys Pro Arg Gly
40 45 50

Val Gln Xaa Leu Met Ile Ser Ile Ser Glu His Leu Phe Ile His Ala
55 60 65 70

```

## (2) INFORMATION FOR SEQ ID NO: 581:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq RWWCFHLQAEASA/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

```

Met Gly Trp Gln Arg Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser
-15 -10 -5

Ala His Pro Pro Gln Gly Leu Gln
1 5

```

## (2) INFORMATION FOR SEQ ID NO: 582:



Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe Gly  
20 25 30  
Xaa Arg Glu Gln Ala Glu Xaa Xaa Arg Tyr Phe  
35 40

## (2) INFORMATION FOR SEQ ID NO: 584:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12  
seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr  
-15 -10 -5  
Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln  
1 5 10  
Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro  
15 20 25 30  
Ser Ala Met Tyr Cys Asp Glu Leu  
35

## (2) INFORMATION FOR SEQ ID NO: 585:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 12  
 seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr  
           -15                                  -10                                  -5  
 Ser Gly Gln Tyr Tyr Asp Trp  
           1                                          5

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -18..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 12  
 seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr  
           -15                                  -10                                  -5  
 Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln  
           1                                  5                                  10  
 Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro  
   15                                  20                                  25                                  30  
 Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val  
                                   35                                  40                                  45  
 Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His  
                                   50                                  55                                  60  
 Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Gly  
           65                                  70                                  75

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.9  
seq LLLLLLPFLLYMA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

```
Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro Phe Leu
-20 -15 -10 -5

Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
 1 5 10

Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
 15 20 25

Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
 30 35 40

Gly Ala Arg Val Tyr Xaa Ala Xaa Xaa Asp Val Glu Lys Gly Glu Leu
 45 50 55 60

Val Ala Xaa Glu Ile Gln Thr Thr Thr Gly Xaa Xaa Gln Val Leu Val
 65 70 75

Arg Xaa Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala
 80 85 90
```

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1

seq LLYLLVPALFCRA/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

Met Trp Leu Leu Tyr Leu Leu Val Pro Ala Leu Phe Cys Arg Ala Gly  
 -15 -10 -5 1

Gly Ser Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser Pro  
 5 10 15

Leu Phe Pro Lys Pro Tyr Pro Asn Gly  
 20 25

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq LLFLVAGLLPSFP/AN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

Met Lys Gln Ile Leu His Pro Ala Leu Glu Thr Thr Ala Met Thr Leu  
 -30 -25 -20

Phe Pro Val Leu Leu Phe Leu Val Ala Gly Leu Leu Pro Ser Phe Pro  
 -15 -10 -5

Ala Asn Glu Asp Lys Asp Pro Ala Phe Thr Ala Leu Leu Thr Thr Gln  
 1 5 10 15

Thr Gln Val Gln Arg Glu Ile Val Asn Lys His Asn Glu Leu Arg Arg  
 20 25 30

Ala Val Ser Pro Pro Ala Lys  
 35

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.9  
seq LFLTMLTLALVKS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

```

Met Leu Lys Ala Leu Phe Leu Thr Met Leu Thr Leu Ala Leu Val Lys
 -15 -10 -5
Ser Gln Asp Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly
 1 5 10 15
Tyr Glu Trp Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys
 20 25 30
Asp Ile Val Pro Asp Ala Cys Lys Gly Gly Met Lys Cys Val Asn His
 35 40 45
Tyr Gly Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn
 50 55 60
Asn Glu Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly
 65 70 75
Ala Thr Thr Gly Val Val Ala Ala Xaa Ser Met Ala Thr Ser Xaa Val
 80 85 90 95
Leu Xaa Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro
 100 105 110
Glu Met Gln Thr Gly Arg Asn Asn Phe Val
 115 120

```

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:



(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -22..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.9  
 seq LLILWFHLDCVSS/IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

```

Met Glu Lys Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His
 -20 -15 -10

Leu Asp Cys Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser
 -5 1 5 10

Leu His Val Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro
 15 20 25

Ser Ser Asn Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys
 30 35 40

Ser Pro Glu Ala Val
 45

```

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -15..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.3  
 seq VVTIVILLCFCKA/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

```

Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala
-15 -10 -5 1

Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His
 5 10 15

Gly Arg Ala Gly Gly
 20

```

(2) INFORMATION FOR SEQ ID NO: 593:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -90..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq LLFVATLPFWTHY/LI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

```

Met Asp Gln Phe Pro Glu Ser Val Thr Glu Asn Phe Glu Tyr Asp Asp
-90 -85 -80 -75

Leu Ala Glu Ala Cys Tyr Ile Gly Asp Ile Val Val Phe Gly Thr Val
 -70 -65 -60

Phe Leu Ser Ile Phe Tyr Ser Val Ile Phe Ala Ile Gly Leu Val Gly
 -55 -50 -45

Asn Leu Leu Val Val Phe Ala Leu Thr Asn Ser Lys Lys Pro Lys Ser
 -40 -35 -30

Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Leu Ser Asp Leu Leu Phe
 -25 -20 -15

Val Ala Thr Leu Pro Phe Trp Thr His Tyr Leu Ile Asn Glu Lys Gly
-10 -5 1 5

Leu His Asn Ala Met Cys
 -10

```